

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 4, 2004, 14:18:01 / Search time 21 Seconds  
(without alignments)  
689,063 Million cell updates/sec

Title: US-09-780-576-2

Perfect score: 1778  
Sequence: 1 MOAVDNLTSAPGNTSLCTRD.....SQDNKKKQGGGDPNEETPM 342

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/5C\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/5D\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/5E\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/5F\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1778	100.0	342	US-08-852-824-2	Sequence 2, Appl
2	823	46.3	333	US-09-221-456-2	Sequence 2, Appl
3	823	46.3	333	US-09-558-740-2	Sequence 2, Appl
4	797	44.8	333	US-08-812-871-1	Sequence 1, Appl
5	772	43.4	325	US-08-467-948A-29	Sequence 29, Appl
6	772	43.4	325	US-08-467-947A-29	Sequence 29, Appl
7	772	43.4	338	US-08-988-876-8	Sequence 8, Appl
8	772	43.4	338	US-08-303-524A-2	Sequence 2, Appl
9	679.5	38.2	358	US-08-988-876-3	Sequence 3, Appl
10	546.5	30.7	293	US-08-467-948A-6	Sequence 6, Appl
11	546.5	30.7	293	US-08-467-947A-6	Sequence 6, Appl
12	488	27.4	319	US-08-702-344-28	Sequence 28, Appl
13	410.5	23.1	326	US-08-118-270-32	Sequence 32, Appl
14	410.5	23.1	326	PCT-US93-08528-39	Sequence 39, Appl
15	392.5	22.1	342	US-08-988-876-9	Sequence 9, Appl
16	379.5	21.3	361	US-08-383-750-4	Sequence 4, Appl
17	379.5	21.3	361	US-08-352-678-4	Sequence 4, Appl
18	379.5	21.3	361	US-09-536-954-4	Sequence 4, Appl
19	379.5	21.3	361	US-09-170-496D-78	Sequence 78, Appl
20	379.5	21.3	361	US-09-170-496D-206	Sequence 206, Appl
21	379.5	21.3	361	PCT-US93-09636-4	Sequence 4, Appl
22	378	21.3	316	US-09-690-454-69	Sequence 69, Appl
23	376	21.1	346	US-08-852-824-17	Sequence 17, Appl
24	374.5	21.1	381	US-08-467-125-2	Sequence 2, Appl
25	374.5	21.1	381	US-08-911-320A-2	Sequence 2, Appl
26	374.5	21.1	381	US-09-217-101-2	Sequence 2, Appl
27	349.5	19.7	302	US-08-467-948A-30	Sequence 30, Appl

28	349.5	19.7	302	US-08-467-947A-30	Sequence 30, Appl
29	347.5	19.5	346	US-09-585-876-2	Sequence 2, Appl
30	339	19.1	344	US-08-467-948A-8	Sequence 8, Appl
31	339	19.1	344	US-08-467-947A-8	Sequence 8, Appl
32	337	19.0	68	US-08-905-223-327	Sequence 327, App
33	332.5	18.7	339	US-09-170-496D-182	Sequence 182, App
34	329.5	18.5	339	US-08-153-848-44	Sequence 44, Appl
35	329.5	18.5	339	US-08-812-871-3	Sequence 3, Appl
36	329.5	18.5	339	US-09-299-843A-44	Sequence 44, Appl
37	329.5	18.5	339	US-09-088-337B-44	Sequence 44, Appl
38	329.5	18.5	339	US-09-170-496D-32	Sequence 32, Appl
39	329.5	18.5	339	US-09-1153-44	Sequence 44, Appl
40	329.5	18.5	339	PCT-US93-07180-2	Sequence 2, Appl
41	329	18.5	359	US-08-041-219A-6	Sequence 6, Appl
42	329	18.5	359	US-08-417-122-6	Sequence 6, Appl
43	327.5	18.4	395	US-08-097-938-2	Sequence 2, Appl
44	327.5	18.4	395	US-08-476-000-2	Sequence 2, Appl
45	327.5	18.4	395	US-08-472-840-2	Sequence 2, Appl

## ALIGNMENTS

RESULT 1  
US-08-852-824-2  
Sequence 2, Application US/08852824C  
Patent No. 6060272  
GENERAL INFORMATION:  
APPLICANT: Li et al.  
TITLE OF INVENTION: Human G-Protein Coupled Receptors  
FILE REFERENCE: 1488.1220000  
CURRENT APPLICATION NUMBER: US/08/852,824C  
CURRENT FILING DATE: 1997-05-04  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 342  
TYPE: PRT  
ORGANISM: Genomic  
US-08-852-824-2

Query Match 100.0%; Score 1778; DB 3; Length 342;

Best Local Similarity 100.0%; Pred. No. 2.4e-144; Indels 0; Gaps 0;

Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MOAVDNLTSAPGNTSLCTRDYKIQVLPFLITYVLFVGLITNGLAMRIFPOIRKSNFI	60
DB	1	MOAVDNLTSAPGNTSLCTRDYKIQVLPFLITYVLFVGLITNGLAMRIFPOIRKSNFI	60
QY	61	IFLKNTVSDLMITPPKLSDAKGTGGLTFVQCVSVIFPTMYISIFLGLITI	120
DB	61	IFLKNTVSDLMITPPKLSDAKGTGGLTFVQCVSVIFPTMYISIFLGLITI	120
QY	121	DEYQKTRPPKTSNEKNLGAKLISVIMAFMFLISPMILITNRQPDKNVKKCSPLKS	180
DB	121	DEYQKTRPPKTSNEKNLGAKLISVIMAFMFLISPMILITNRQPDKNVKKCSPLKS	180
QY	181	BEGLYMHETVNTICVITWIFLVIVCYTILITELVRSYRTGVGVPPKKNVXFEI	240
DB	181	BEGLYMHETVNTICVITWIFLVIVCYTILITELVRSYRTGVGVPPKKNVXFEI	240
QY	241	IIAVFFICVPHFARIPYTLISQTEVDVCTAENLTFYKESITLMTLSINACDPIFYF	300
DB	241	IIAVFFICVPHFARIPYTLISQTEVDVCTAENLTFYKESITLMTLSINACDPIFYF	300
QY	301	LCKSPRNSLISLWKCPNSATSLSQDNKKKQGGGDPNEETPM 342	
DB	301	LCKSPRNSLISLWKCPNSATSLSQDNKKKQGGGDPNEETPM 342	

RESULT 2  
US-09-221-456-2  
Sequence 2, Application US/09221456

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; Patent No. 6162899
; GENERAL INFORMATION:
; APPLICANT: SATHE, GANESH
; APPLICANT: HALSEY, WENDY
; APPLICANT: MUIR, ALISON
; APPLICANT: CHAMBERS, JON
; APPLICANT: SZEKERES, PHILIP
; TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS
; TITLE OF INVENTION: AND ANTAGONISTS OF THE HNEAA81 RECEPTOR
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: PastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/221,456
; FILING DATE: 28-DEC-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/956,975
; FILING DATE: 23-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70318-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0700
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 333 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-221-456-2

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Query Match 46.3%; Score 823; DB 3; Length 333;
Best Local Similarity 48.7%; Pred. No. 7.6e-63;
Matches 154; Conservative 57; Mismatches 103; Indels 2; Gaps 1;

QY 17 CTRDYKIQVLPFLYTVLFFVGLITNGLAMRIFFOIRKSNPFIIFLKNVTISDLIMILT 76
DB 15 CPDRTRIVQLVFPALYTVVLTGILLNTLALWVHVHPSSSTFIIVLKNVLVADLIMLTLM 74

QY 77 FPFKILSDAKLGTGPTLFTVCQVTSVIFYFTMTWISIFLGLITIDRYOKTRPFKTSNPK 136
DB 75 LPFKILSDSHLAPWQRAFAVCRFSSVIFYFTMTWISIFLGLITIDRYOKTRPFKTSNPK 134

QY 137 NLLGAKILSVVIWAFMFLSLPNMILNPRODNKVKCSFLKSEFGLVWHEIVNYICQV 196
DB 135 KPVFAKTVSIFWFLFPIISLNTILNKEATSSVKKCSLKGPLGKWHQVNNICQF 194

QY 197 IFWNLFLIVVCYTLITKELYSYRVRGVKVPKKNVKKVFIITAVFFICVPHFAR 256
DB 195 IFWTVFILMLVYVVIKAVYDSYRKSVDKKNKKLGGKVFVWVAVFVCFAPHFAR 254

QY 257 IPYTLSDQTRDVFDCATNTLFFVKESTLMTLSNACLDPRIFVFLCKSPFNLSMLKCP 316
DB 255 VPYTHSQTNKTDCLQNQLFIKATETLFLAATNIMDPLIYIFLCKKFTKLPCHQ--G 312

QY 317 NSATSLSQDNKKEQD 332
DB 313 RKTASSQENHSSQTD 328

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RESULT 4

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US-08-812-871-1
; Sequence 1, Application US/08812871
; Patent No. 5955303
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Guegler, Karl
; APPLICANT: Muzong Cheng
; TITLE OF INVENTION: NOVEL HUMAN CHEMOKINE RECEPTOR-LIKE
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto

```

```

RESULT 3
US-09-558-740-2
; Sequence 2, Application US/09558740
; Patent No. 6358695
; GENERAL INFORMATION:
; APPLICANT: SATHE, GANESH
; APPLICANT: HALSEY, WENDY
; APPLICANT: MUIR, ALISON
; APPLICANT: CHAMBERS, JON
; APPLICANT: SZEKERES, PHILIP
; TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS AND
; TITLE OF INVENTION: ANTAGONISTS OF THE HNEAA81 RECEPTOR
; FILE REFERENCE: GH-70318-2
; CURRENT APPLICATION NUMBER: US/09/558,740
; CURRENT FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 08/956,975
; PRIOR FILING DATE: 1997-10-23
; PRIOR APPLICATION NUMBER: 09/221,456
; PRIOR FILING DATE: 1998-12-28
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 333
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; US-09-558-740-2

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Query Match 46.3%; Score 823; DB 4; Length 333;
Best Local Similarity 48.7%; Pred. No. 7.6e-63;
Matches 154; Conservative 57; Mismatches 103; Indels 2; Gaps 1;

QY 17 CTRDYKIQVLPFLYTVLFFVGLITNGLAMRIFFOIRKSNPFIIFLKNVTISDLIMILT 76
DB 15 CPDRTRIVQLVFPALYTVVLTGILLNTLALWVHVHPSSSTFIIVLKNVLVADLIMLTLM 74

QY 77 FPFKILSDAKLGTGPTLFTVCQVTSVIFYFTMTWISIFLGLITIDRYOKTRPFKTSNPK 136
DB 75 LPFKILSDSHLAPWQRAFAVCRFSSVIFYFTMTWISIFLGLITIDRYOKTRPFKTSNPK 134

QY 137 NLLGAKILSVVIWAFMFLSLPNMILNPRODNKVKCSFLKSEFGLVWHEIVNYICQV 196
DB 135 KPVFAKTVSIFWFLFPIISLNTILNKEATSSVKKCSLKGPLGKWHQVNNICQF 194

QY 197 IFWNLFLIVVCYTLITKELYSYRVRGVKVPKKNVKKVFIITAVFFICVPHFAR 256
DB 195 IFWTVFILMLVYVVIKAVYDSYRKSVDKKNKKLGGKVFVWVAVFVCFAPHFAR 254

QY 257 IPYTLSDQTRDVFDCATNTLFFVKESTLMTLSNACLDPRIFVFLCKSPFNLSMLKCP 316
DB 255 VPYTHSQTNKTDCLQNQLFIKATETLFLAATNIMDPLIYIFLCKKFTKLPCHQ--G 312

QY 317 NSATSLSQDNKKEQD 332
DB 313 RKTASSQENHSSQTD 328

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STATE: CA  
 COUNTRY: USA  
 ZIP: 94304  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSO for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/812,871  
 FILING DATE: Filed Herewith  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 NAME: Billings, Lucy J  
 REGISTRATION NUMBER: 36,749  
 REFERENCE/DOCKET NUMBER: PF-0237 US  
 TELEPHONE: 415-855-0555  
 TELEFAX: 415-845-4166  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 333 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 IMMEDIATE SOURCE:  
 LIBRARY: MMLR3DT01  
 CLONE: 568987  
 US-08-812-871-1

Query Match 44.8%; Score 797; DB 2; Length 333;

Best Local Similarity 47.8%; Pred. No. 1.3e-60;

Matches 151; Conservative 57; Mismatches 106; Indels 2; Gaps 1;

QY 17 CTRDYKLTQVLPFLYLVLFVGLITNGLAMRIFFOIRKSNFIILKNTVLSLLMILT 76  
 DB 15 CPDRTRIVQVLFALYFVFLTGILNTLALWVFVHPSSFTIILKNTLVADLIMLT 74  
 QY 77 FPKILSDAKLGTGPLATFVCQVTSVIFYETMYISIFLGLITIDRYQKTRPPFKTSNPK 136  
 DB 75 LPPKILSDSLAPQLRAFCRFSSVIFYETMYVIGVLLGLIAFDRLKIIRPLRNIFLK 134  
 QY 137 NLGAKILSVIVAFWFLSLPMLTNRQPRDNVKKCSFLKSEGLVWHEIVNYICQV 196  
 DB 135 KPVFAKTVSIFVFFLFFISLPIMLSNKEATPSSVKKCASLKGPLGLKWKHQWNNICQF 194  
 QY 197 IFWNLFLIVVCVTLITKELYRSYVTRGVGKVRPKKVNKVFIIIAVFFICFVPFHFAR 256  
 DB 195 IFWVTLMLVYVVIKAYVDSYKSKCKDRKNNKLBGVFVVVVFVCFAPFHFAR 254  
 QY 257 IPYTLSDTRDVEDCTAENTLFYKVESTLMTSLNACLDPPIYFLCKSPRNSLISMLKCP 316  
 DB 255 VPYTHSTNNKTDCLQNLQFLIAKETTLFLAATNICMDPLISIFLCKKTEKLPCMQ--G 312  
 QY 317 NSATLSQDNKKKEQD 332  
 DB 313 RKTASSQENHSSQTD 328

# RESULT 5

US-08-467-948A-29

; Sequence 29, Application US/08467948A

; Patent No. 5998164

; GENERAL INFORMATION:

; APPLICANT: LI, YI

; APPLICANT: CAO, LIANG

; APPLICANT: NI, JIAN

; APPLICANT: GENTZ, REINER

; APPLICANT: BULT, CAROL J.

; APPLICANT: SUTTON III, GRANGER G.

APPLICANT: ROSEN, CRAIG A.  
 TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein  
 TITLE OF INVENTION: Coupled Receptor GPR2  
 NUMBER OF SEQUENCES: 30  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
 STREET: 1100 NEW YORK AVE., NW, SUITE 600  
 CITY: WASHINGTON  
 STATE: DC  
 COUNTRY: USA  
 ZIP: 20005  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY DISK  
 COMPUTER: IBM PC COMPATIBLE  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/467,948A  
 FILING DATE: 06-JUN-1995  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US95/04079  
 FILING DATE: 30-MAR-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: STEFFE, ERIC K.  
 REGISTRATION NUMBER: 36,688  
 REFERENCE/DOCKET NUMBER: 1488.1140003/EKS/KLM  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-371-2600  
 TELEFAX: 202-371-2540  
 INFORMATION FOR SEQ ID NO: 29:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 325 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: not relevant  
 MOLECULE TYPE: peptide  
 US-08-467-948A-29

Query Match 43.4%; Score 772; DB 2; Length 325;

Best Local Similarity 47.5%; Pred. No. 1.7e-58;

Matches 149; Conservative 60; Mismatches 105; Indels 0; Gaps 0;

QY 6 NLTSAPGNSTLCTRDYKITQVLPFLYLVLFVGLITNGLAMRIFFOIRKSNPIILKLN 65  
 DB 2 NSTQTPDSDSCSNLIITQIIPVLYCWVFIAGILNGVGHIFVFPSSKSPILVKN 61  
 QY 66 TVISDLMLITFPFKILSDAKLGTGPLRTFVCQVTSVIFYETMYISIFLGLITIDRYOK 125  
 DB 62 IVIADFVMSLTFPPKILGDSGLGPWQLNVFVCRVSAVLFVYNNYKSVIVFFGLISFDYYK 121  
 QY 126 TTRPFTSNPKNLGAKILSVIWAFFWFLSLPMLTNRQPRDNVKKCSFLKSEFGLV 185  
 DB 122 IVKPLWTFQTSVYSKLLSVIWMMLLAVFNILITNOSVREVTOIKIELKSELGRK 181  
 QY 186 WHEIVNYICQVIFWNLFLIVVCVTLITKELYRSYVTRGVGKVRPKKVNKVFIIIAV 245  
 DB 182 WKASNYIFVAIFWVFLILLIVFYTAITKKIFKSHLKSNNSTSVKCKSRNIFSVFVF 241  
 QY 246 PICVFPFHARIPYTLSDTRDVEDCTAENTLFYKVESTLMTSLNACLDPPIYFLCKSP 305  
 DB 242 FVCFVPVPHARIPYTKSQTEAHVSCQSKETLRVWKEFTLLLSAANVCLDPIIYFLCKSP 301

# RESULT 6

US-08-467-947A-29

; Sequence 29, Application US/08467947A

; Patent No. 6090575

; GENERAL INFORMATION:

; APPLICANT: SUTTON III, GRANGER G.

APPLICANT: LI, YI  
APPLICANT: CAO, LIANG  
APPLICANT: NI, JIAN  
APPLICANT: GENTZ, REINER  
APPLICANT: BULT, CAROL J.  
APPLICANT: SUTTON III, GRANGER G.  
APPLICANT: ROSEN, CRAIG A.  
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein  
TITLE OF INVENTION: Coupled Receptor GPR1  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 NEW YORK AVE., NW, SUITE 600  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,947A  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION NUMBER: PCT/US95/04079  
FILING DATE: 30-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: STEFFE, ERIC K.  
REGISTRATION NUMBER: 36,688  
REFERENCE/DOCKET NUMBER: 1488.1140002/EKS/KUM  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 325 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: not relevant  
MOLECULE TYPE: peptide  
US-08-467-947A-29

Query Match 43.4%; Score 772; DB 3; Length 325;  
Best Local Similarity 47.5%; Pred. No. 1.7e-58;  
Matches 149; Conservative 60; Mismatches 105; Indels 0; Gaps 0;

QY 6 NLTSAPGNTSLCTRDYKLTQVLPFLYTVLFFVGLITNGLAMRIFPQIRSKSNFIILKN 65  
DB 2 NSTSTQPPDESCQNLLITQOIIPVLCVNFVFIAGLLNGVSGWIFFYVPSSKSFIIYLN 61  
QY 66 TVISDLMLITPFPKILSDAKLGTGPLERTFVCQVTSVIFFTMYISISFLGLITIDRYOK 125  
DB 62 IVIADPFWMSLTFFPKILGSDGLGPMQLANFVCRVSAVLFYVNMYSIVFFGLISFDYYK 121  
QY 126 TTRPFTKSNPKLLGAKILSVIWMFLLSPNMLITNRQPRDKNVKCSFLKSEFGLV 185  
DB 122 IVKPLMTSFTQSVYSKLSVIVWMLLAVPNILITNQSVREVTOIKIELKSELGRK 181  
QY 186 WHEIVNYICQVIFWIFNFIIVCYTILITKELYSRVYRTRGVGKVPKKNVKKVFIILAVF 245  
DB 182 WHKASNYIFVAIFWIFVFLIIIVFYTAITKKIFKSHLKSSRNSTSVKKSRRNIFSVFVF 241  
QY 246 FICFVPHFARIPTLTLSQTRDVFDCFTAENTLFWKESITLWLTSLNACLDPPFYPLCKSF 305  
DB 242 FVCVPHIARIPTLTLSQTRDVFDCFTAENTLFWKESITLWLTSLNACLDPPFYPLCKSF 301  
QY 306 RNSLISMLKCPNSA 319  
DB 302 REILCKKLIPLKA 315

RESULT 7  
US-08-988-876-8  
; Sequence 8, Application US/08988876  
; Patent No. 6063596  
; GENERAL INFORMATION:  
; APPLICANT: Lal, Preeti  
; APPLICANT: Bandman, Olga  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Yue, Henry  
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED  
; TITLE OF INVENTION: WITH IMMUNE RESPONSE  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/988,876  
; FILING DATE: Herewith  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0441 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-855-0555  
; TELEFAX: 650-845-4166  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 338 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GenBank  
; CLONE: 285995  
; US-08-988-876-8

Query Match 43.4%; Score 772; DB 3; Length 338;  
Best Local Similarity 47.5%; Pred. No. 1.7e-58;  
Matches 149; Conservative 60; Mismatches 105; Indels 0; Gaps 0;

QY 6 NLTSAPGNTSLCTRDYKLTQVLPFLYTVLFFVGLITNGLAMRIFPQIRSKSNFIILKN 65  
DB 3 NSTSTQPPDESCQNLLITQOIIPVLCVNFVFIAGLLNGVSGWIFFYVPSSKSFIIYLN 62  
QY 66 TVISDLMLITPFPKILSDAKLGTGPLERTFVCQVTSVIFFTMYISISFLGLITIDRYOK 125  
DB 63 IVIADPFWMSLTFFPKILGSDGLGPMQLANFVCRVSAVLFYVNMYSIVFFGLISFDYYK 122  
QY 126 TTRPFTKSNPKLLGAKILSVIWMFLLSPNMLITNRQPRDKNVKCSFLKSEFGLV 185  
DB 122 IVKPLMTSFTQSVYSKLSVIVWMLLAVPNILITNQSVREVTOIKIELKSELGRK 182  
QY 186 WHEIVNYICQVIFWIFNFIIVCYTILITKELYSRVYRTRGVGKVPKKNVKKVFIILAVF 245  
DB 183 WHKASNYIFVAIFWIFVFLIIIVFYTAITKKIFKSHLKSSRNSTSVKKSRRNIFSVFVF 242  
QY 246 FICFVPHFARIPTLTLSQTRDVFDCFTAENTLFWKESITLWLTSLNACLDPPFYPLCKSF 305

Db 243 FVCVPYHARIPTKQTEAHYSCQSEILRYMKEFTLLLSAANVCLDPIIYFLLCQPF 302  
 Qy 306 RNSLSMLKCPNSA 319  
 Db 303 REILCKKLHIPLKA 316

RESULT 8

US-09-303-524A-2  
 ; Sequence 2, Application US/09303524A  
 ; Patent No. 6238873  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CHAMBERS, JONATHAN K.  
 ; APPLICANT: STEWART, BRIAN R.  
 ; APPLICANT: AMES, ROBERT S.  
 ; APPLICANT: SARAU, HENRY M.  
 ; APPLICANT: FOLEY, JIM  
 ; APPLICANT: ARNOLD, ANNE ROMANIC  
 ; TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS AND  
 ; ANTAGONISTS OF THE INTERACTION BETWEEN THE HUMAN KIAA0001  
 ; TITLE OF INVENTION: RECEPTOR AND LIGANDS THEREOF  
 ; FILE REFERENCE: GP50007  
 ; CURRENT APPLICATION NUMBER: US/09/303,524A  
 ; CURRENT FILING DATE: 1999-04-30  
 ; PRIOR APPLICATION NUMBER: 60/083,957  
 ; PRIOR FILING DATE: 1998-05-01  
 ; NUMBER OF SEQ ID NOS: 2  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO: 2  
 ; LENGTH: 338  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-303-524A-2

Query Match 43.4%; Score 772; DB 3; Length 338;  
 Best Local Similarity 47.5%; Pred. No. 1.7e-58;  
 Matches 149; Conservative 60; Mismatches 105; Indels 0; Gaps 0;

Qy 6 NLTSAPGNTSLCTRDYKITQVLFPVLYLVLPVGLITNGLAMRFPQIRSKSNFIILKXN 65  
 Db 3 NSTSQPPDESQNLITQIIPVLCVFIAGILLNGVSGWIFFYVPSSKSPFIILKXN 62  
 Qy 66 TVISDLMLTPFPKILSDAKLGTGTLRTFVCQVTSVIFFTWISISFLGLITIDRYQK 125  
 Db 63 IVIAFVMSLTPFPKILSDGLGPGQNLVFCVRSVAVLFYNNMYSIVFGLISFDRYK 122  
 Qy 126 TTRPPTSNPKNLLGAKILSVVIAFMFLLSLPNNMILTNQPRDKNVKCKSFLKSEFGLV 185  
 Db 123 IVKPLWTSFISQSVSKLSLVIVVMMLLAVPNIILTNQSVREVTQIKCIELKSELGRK 182  
 Qy 186 WHEIYNYICQVIFWNLIVIVCVTLITKELYSVYTRGVGVKPKVNVKVFIIIAVF 245  
 Db 183 WHKASNYIFVAIFWNLIVIVCVTLITKELYSVYTRGVGVKPKVNVKVFIIIAVF 242  
 Qy 246 FICFVFPFHARIPYTLQSTRDVEDCTAENTLFFYKSESTLWLTSLNACLDPIIYFLLCKSF 305  
 Db 243 FVCVPYHARIPTKQTEAHYSCQSEILRYMKEFTLLLSAANVCLDPIIYFLLCQPF 302  
 Qy 306 RNSLSMLKCPNSA 319  
 Db 303 REILCKKLHIPLKA 316

RESULT 9

US-08-988-876-3  
 ; Sequence 3, Application US/08988876  
 ; Patent No. 6063596  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lal, Preeti  
 ; APPLICANT: Bandman, Olga  
 ; APPLICANT: Hillman, Jennifer L.  
 ; APPLICANT: Yue, Henry

; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED  
 ; TITLE OF INVENTION: WITH IMMUNE RESPONSE  
 ; NUMBER OF SEQUENCES: 9  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 ; STREET: 3174 Porter Drive  
 ; CITY: Palo Alto  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 94304  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSeq for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/988,876  
 ; FILING DATE: Herewith  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Billings, Lucy J.  
 ; REGISTRATION NUMBER: 36,749  
 ; REFERENCE/DOCKET NUMBER: PF-0441 US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 650-855-0555  
 ; TELEFAX: 650-845-4166  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 3:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 358 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; IMMEDIATE SOURCE:  
 ; LIBRARY: PROSTUT09  
 ; CLONE: 1650519  
 ; US-08-988-876-3

Query Match 38.2%; Score 679.5; DB 3; Length 358;  
 Best Local Similarity 43.7%; Pred. No. 1.4e-50;  
 Matches 132; Conservative 64; Mismatches 99; Indels 7; Gaps 4;

Qy 6 NLTSAPG-NTSLCTRDYKITQVLFPVLYLVLPVGLITNGLAMRFPQIRSKSNFIILK 64  
 Db 25 NRSDFGKNTLL--HNEPDTIVLPVLYLIFVASILLNGLAVWIFFHIRNKTSIFVYK 81  
 Qy 65 NTVISDLMLTPFPKILSDAKLGTGTLRTFVCQVTSVIFFTWISISFLGLITIDRYQ 124  
 Db 82 NIYVADLIMTLTFFPRIVHDAGFGPWYFKILCRYTSLFYANMYTSIVFLGLISIDRYL 141  
 Qy 125 KTRPPTSNPKNLLGAKILSVVIAFMFLLSLPNNMILTNQPRDKNVKCKSFLKSEFGL 184  
 Db 142 KVKPFGDGRMYSIFTKVLSVCVVMIAVLSLPNILLTNGQPTEDNHDCKSLKSLGV 201  
 Qy 185 WHEIYNYICQVIFWNLIVIVCVTLITKELYSVYTRGVGVKPKV-NNVNVFIIIA 243  
 Db 202 KWHATVYVNSCLFVAVLVILICVTAISRYTHKS--SQFISQSRRKKNQSRVWA 259  
 Qy 244 VFFICFVFPFHARIPYTLQSTRDVEDCTAENTLFFYKSESTLWLTSLNACLDPIIYFLLCK 303  
 Db 260 VYFTCLPVLHLCMPSTFSLDRLLDESQKILYYCKEITLFLSACNVCLDPIIYFLLCK 319  
 Qy 304 SF 305  
 Db 320 SF 321

RESULT 10  
 US-08-467-948A-6  
 ; Sequence 6, Application US/08467948A

Patent No. 5998164  
GENERAL INFORMATION:  
APPLICANT: LI, YI  
APPLICANT: CAO, LIANG  
APPLICANT: NI, JIAN  
APPLICANT: GENTZ, REINER  
APPLICANT: BULT, CAROL J.  
APPLICANT: SUTTON III, GRANGER G.  
APPLICANT: ROSEN, CRAIG A.  
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein  
TITLE OF INVENTION: Coupled Receptor GPR2  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 NEW YORK AVE., NW, SUITE 600  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,948A  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/04079  
FILING DATE: 30-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: STEFFE, ERIC K.  
REGISTRATION NUMBER: 36,688  
REFERENCE/DOCKET NUMBER: 1488.1140003/EKS/KLM  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 293 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-467-948A-6

Query Match 30.7%; Score 546.5; DB 2; Length 293;  
Best Local Similarity 42.3%; Pred. No. 2.6e-39;  
Matches 116; Conservative 45; Mismatches 104; Indels 9; Gaps 4;  
QY 17 CTRDYKITQVLPFLTYLVLFVGLITNGLAMRIFFQIRSKSNFIIFLKNVTISDLMLILT 76  
DB 15 CPKDTRIQVLPFLTYLVLFVGLITNGLAMRIFFQIRSKSNFIIFLKNVTISDLMLILT 74  
QY 77 FPKILSDAKLGTGLRTFCVQTSVIFVFTMYISISFLGLITIDRYOKTTRPFKTSNPK 136  
DB 75 LPFKILSDHSLAPQWLRARVCFSSVIFVFTMYISISFLGLITIDRYOKTTRPFKTSNPK 134  
QY 137 NLIGAKILSVVIAWAFMLLSLPNMLITNRPDKKNVKCSFLKSEFGLVWHEIVNYICQV 196  
DB 135 KPWVGKTVSIFVFWFFISLPNMLISNKEATPSSVKKCSLKGFLGKWKHQMWNICQF 194  
QY 197 IFWINEFLIVVCVLTITKE-----LYRSYVTRGVGVKPKKNVVFIIIAVFFICFVP- 251  
DB 195 IFWTVFILLMVFVYVIAKKYIMILIESPKVTRTKTSWKAKYLLSWLSLCLVLLHFISPE 254  
QY 252 FHPARIPYILSOTRDVFDCTAENTLIFYVKESTLW 285  
DB 255 FHILTVPKPIRLT---VDCKI-NCILLKKQLSFW 284

RESULT 11  
US-08-467-947A-6

Sequence 6, Application US/08467947A  
Patent No. 6090575  
GENERAL INFORMATION:  
APPLICANT: LI, YI  
APPLICANT: CAO, LIANG  
APPLICANT: NI, JIAN  
APPLICANT: GENTZ, REINER  
APPLICANT: BULT, CAROL J.  
APPLICANT: SUTTON III, GRANGER G.  
APPLICANT: ROSEN, CRAIG A.  
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein  
TITLE OF INVENTION: Coupled Receptor GPR1  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 NEW YORK AVE., NW, SUITE 600  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,947A  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/04079  
FILING DATE: 30-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: STEFFE, ERIC K.  
REGISTRATION NUMBER: 36,688  
REFERENCE/DOCKET NUMBER: 1488.1140002/EKS/KLM  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 293 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-467-947A-6

Query Match 30.7%; Score 546.5; DB 3; Length 293;  
Best Local Similarity 42.3%; Pred. No. 2.6e-39;  
Matches 116; Conservative 45; Mismatches 104; Indels 9; Gaps 4;  
QY 17 CTRDYKITQVLPFLTYLVLFVGLITNGLAMRIFFQIRSKSNFIIFLKNVTISDLMLILT 76  
DB 15 CPKDTRIQVLPFLTYLVLFVGLITNGLAMRIFFQIRSKSNFIIFLKNVTISDLMLILT 74  
QY 77 FPKILSDAKLGTGLRTFCVQTSVIFVFTMYISISFLGLITIDRYOKTTRPFKTSNPK 136  
DB 75 LPFKILSDHSLAPQWLRARVCFSSVIFVFTMYISISFLGLITIDRYOKTTRPFKTSNPK 134  
QY 137 NLIGAKILSVVIAWAFMLLSLPNMLITNRPDKKNVKCSFLKSEFGLVWHEIVNYICQV 196  
DB 135 KPWVGKTVSIFVFWFFISLPNMLISNKEATPSSVKKCSLKGFLGKWKHQMWNICQF 194  
QY 197 IFWINEFLIVVCVLTITKE-----LYRSYVTRGVGVKPKKNVVFIIIAVFFICFVP- 251  
DB 195 IFWTVFILLMVFVYVIAKKYIMILIESPKVTRTKTSWKAKYLLSWLSLCLVLLHFISPE 254  
QY 252 FHPARIPYILSOTRDVFDCTAENTLIFYVKESTLW 285  
DB 255 FHILTVPKPIRLT---VDCKI-NCILLKKQLSFW 284

RESULT 12

US-08-702-344-28

; Sequence 28, Application US/08702344

; Patent No. 5723315

; GENERAL INFORMATION:

; APPLICANT: Jacobs, Kenneth

; APPLICANT: McCoy, John

; APPLICANT: Lavalie, Edward

; APPLICANT: Racie, Lisa

; APPLICANT: Merberg, David

; APPLICANT: Treacy, Maurice

; APPLICANT: Spaulding, Vikki

; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES

; TITLE OF INVENTION: ENCODING THEM

; NUMBER OF SEQUENCES: 37

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genetics Institute, Inc.

; STREET: 87 CambridgePark Drive

; CITY: Cambridge

; STATE: Massachusetts

; COUNTRY: U.S.A.

; ZIP: 02140

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.30

; CURRENT APPLICATION DATA: US/08/702,344

; FILING DATE:

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: Brown, Scott A.

; REGISTRATION NUMBER: 32,724

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 498-8224

; TELEFAX: (617) 876-5851

; INFORMATION FOR SEQ ID NO: 28:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 319 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-702-344-28

Query Match

Best Local Similarity 27.4%; Score 488; DB 1; Length 319;

Matches 112; Conservative 62; Mismatches 125; Indels 26; Gaps 9;

QY 13 NTSCTRDYKIQVLPFLLYTVLFFVGLITNGLAMRIFPQIRSKNFI-IFLKNVTISDL 71

Db 3 NSSPFCVPYKOLEP-FYFFYLVFLVGIIGSCFATWAFIQKTNHRCVSIYLLNLTA 61

QY 72 LMLTFFPKILSDAKLTGP--LRTFVCQVTSVIFFTWYISIFLGLITIDRYQKTRP 129

Db 52 LTLALPKIWD--LGVAPEKLFICQVTAFLIYNNVLSIFLAFVSDICLQIHTS 119

QY 130 FKTSPKXNLGAKILSVVWAFMFLSLPNMILTNQPRDKNVKCSFLKSPGLVWHEI 189

Db 120 CKYRIQEPGFAKIMISTVWMLWLLIMVPPNMIPIKDIKEKSNVGMCFKKEFGRNWHL 179

QY 190 VNYICQVIFWNE-LIVIVCVTLITKELYSYVTRGVKVR-KKNVNVKVFIIIAVEPI 247

Db 180 TNFICVAIP-LNFSAILIISNCLVIQLYRN---KQENYPNVKKALINILVTTGYII 234

QY 248 CFVPPHFARIPYTLISQTRDVEDCTAENTLFYVKESTLWLTSLNACLDPPFYFFLCKSPRN 307

Db 235 CFVPHYVIRIPYTLISQTEVIDTDCSTRISLFAKATLLAVSNLCFDPILYHLSKAFRS 294

QY 308 SLI-----SWLKCPNSA 319

Db 295 KVTETFASPKEKAKKELRCENNA 319

RESULT 13

US-08-118-270-39

; Sequence 39, Application US/08118270

; Patent No. 5508384

; GENERAL INFORMATION:

; APPLICANT: Murphy, Randall B.

; APPLICANT: Schuster, David I.

; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN

; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF

; NUMBER OF SEQUENCES: 348

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BROWDY AND NEIMARK

; STREET: 419 Seventh Street, N.W., Suite 300

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/118,270

; FILING DATE: 09-SEP-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/943,236

; FILING DATE: 10-SEP-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Townsend, Kevin G.

; REGISTRATION NUMBER: 34,033

; REFERENCE/DOCKET NUMBER: MURPHY=2A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-628-5197

; TELEFAX: 202-737-3528

; TELEX: 248633

; INFORMATION FOR SEQ ID NO: 39:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 326 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; US-08-118-270-39

Query Match 23.1%; Score 410.5; DB 1; Length 326;

Best Local Similarity 32.2%; Pred. No. 1.2e-27;

Matches 106; Conservative 65; Mismatches 137; Indels 21; Gaps 9;

QY 27 LFPPLYTVLFFVGLITNGLAMRIFFOI-RSKSNFI-IFLKNVTISDLMLITFPFKILSD 84

Db 1 LFPVYISIFVGLITANGVYLVNFAEYLPYKSKNEIKIFMNVNLTIVADLLFTLPLWIVY 60

QY 85 AKLGTPGLRTFVCQVTSVIFFTWYISIFLGLITIDRYQKTRPFTSNPKNLGAKIL 144

Db 61 SNOGNWFLPKFLCNLAGCLFFINTYCSVAFGLVITYRFOAVKPYIKTAQATTKRGIAL 120

QY 145 SVVW-----AFMFLSLPNMILTNQPRDKNVKCSFLKSEFG----LVWHEIVNYIC 194

Db 121 SLVIVVAIVAAASVFLVMDSTNVVSKAGSGNITRC-FERYEKGSKPVLIIH-----IC 174

QY 195 QVI-FWINFLVIVCYTLITKELYSYVTRGVKVRKKNVVKVFLIIAIVFFICFVPEH 253

Db 175 IVLGFFVFLVLIIFCNLVIHTLLRGPVKQORNAEV-RRRALMVCVIAVFCVPHH 233

QY 254 FARIPYTLISQTRDVEDCTAENTLFYVKESTLWLTSLNACLDPPFYFFLCKSPRN 313

Db 234 MVQLPWTIAEL-GWMPSSNHOAINDAHQVTLCLLSTNCVLDPIVYCFLTKKFKHLSEKL 292

QY 314 KCPNSATSLSQDNKKEQDGGDPNEETPM 342

Db 293 NIMRSSQKSRVTRDTGTGTEMAIPINHTEPV 321



RESULT 14

PCT-US93-08528-39  
 ; Sequence 39, Application PC/TUS9308528  
 ; GENERAL INFORMATION:  
 ; APPLICANT: New York University  
 ; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN  
 ; TITLE OF INVENTION: POLYPEPTIDES, AND COMPOSITIONS AND METHODS THEREOF  
 ; NUMBER OF SEQUENCES: 348  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: BROWDY AND NEIMARK  
 ; STREET: 419 Seventh Street, N.W., Suite 300  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20004  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US93/08528  
 ; FILING DATE: 09-SEP-1993  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/943,236  
 ; FILING DATE: 10-SEP-1992  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Townsend, Kevin G.  
 ; REGISTRATION NUMBER: 34,033  
 ; REFERENCE/DOCKET NUMBER: MURPHY=2 PCT  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 202-628-5197  
 ; TELEFAX: 202-737-3528  
 ; TELEX: 248633  
 ; INFORMATION FOR SEQ ID NO: 39:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 326 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; PCT-US93-08528-39

Query Match 23.1%; Score 410.5; DB 5; Length 326;  
 Best Local Similarity 32.2%; Pred. No. 1.2e-27;  
 Matches 106; Conservative 65; Mismatches 137; Indels 21; Gaps 9;  
 QY 27 LPPLLYTVLFFVGLITNGLAMRIFFQI--RKSNSFI--IFLKNTVISDLMLITPPFKILSD 84  
 Db 1 LPPIVYSIIFVLGIITANGYVWVFLVWVFLVWVFLVWVFLVWVFLVWVFLVWVFLVWVFLVWV 60  
 QY 85 AKLGTGRLTFFVCOVTSVIFFTWYISIFLGLITIDRYQKTTTPFKTSNPKNLLGAKIL 144  
 Db 61 SNQGNWFLPKFLCNLAGCLFFINTYCSVAFGLVITVNFQAVKYPKTAQATTKRGIAL 120  
 QY 145 SVVIW-----AFMFLSLPNMLNRPDRKNVKKCSFLKSEFG-----LVWHIVNYIC 194  
 Db 121 SLIVWVAIAAASYFLVWMDSTNVVSNKAGSNTTRC--FEYERKSKPVLIIH-----IC 174  
 QY 195 QVI--FWINFLIVVCTLTITKELYSYVTRGVKVPKKNVKKVFLIIAIVFFICFVPEH 253  
 Db 175 IVLGFVIFVLLIFCNLVIHTLGRPKVQBNAEV--RRALWVCTVIATVFCFVPHH 233  
 QY 254 FARIPYTLQSOTRDVFDCTAENTLFVYKSTLWLTSLNACLDPPFYFFICKSFRNLSIML 313  
 Db 234 MYQLPWTIAEL--GMWPSNHQAINDAHQVTLCLLSTNCVLDPPVICYFLTKKFKHLSKEL 292  
 QY 314 KCPNSATSLSDNRKKEQDGPNETPM 342  
 Db 293 NIMRSSQKCSRVRDTGTGTMAIPINHTPV 321

RESULT 15

US-08-988-876-9  
 ; Sequence 9, Application US/08988876  
 ; Patent No. 6063596  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lal, Preeti  
 ; APPLICANT: Bandman, Olga  
 ; APPLICANT: Hillman, Jennifer L.  
 ; APPLICANT: Yue, Henry  
 ; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED  
 ; TITLE OF INVENTION: WITH IMMUNE RESPONSE  
 ; NUMBER OF SEQUENCES: 9  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 ; STREET: 3174 Porter Drive  
 ; CITY: Palo Alto  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 94304  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSeq for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/988,876  
 ; FILING DATE: Herewith  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Billings, Lucy J.  
 ; REGISTRATION NUMBER: 36,749  
 ; REFERENCE/DOCKET NUMBER: PF-0441 US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 650-855-0555  
 ; TELEFAX: 650-845-4166  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 9:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 342 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; IMMEDIATE SOURCE:  
 ; LIBRARY: GenBank  
 ; CLONE: 49443  
 ; US-08-988-876-9

Query Match 22.1%; Score 392.5; DB 3; Length 342;  
 Best Local Similarity 30.7%; Pred. No. 4.3e-26;  
 Matches 103; Conservative 66; Mismatches 146; Indels 21; Gaps 9;  
 QY 20 DYKITQVLPPLLYTVLFFVGLITNGLAMRIFFQI--RKSNSFI--IFLKNTVISDLMLIT 76  
 Db 10 DSEFRYTLFPVYISIFVLGIITANGYVWVFLVWVFLVWVFLVWVFLVWVFLVWVFLVWVFLVWV 69  
 QY 77 PPFKILSDAKLGTGRLTFFVCOVTSVIFFTWYISIFLGLITIDRYQKTTTPFKTSNPK 136  
 Db 70 LPLWIVVYSNQGWNFLPKFLCNLAGCLFFINTYCSVAFGLVITVNFQAVKYPKTAQAT 129  
 QY 137 NLGAKILSVVIW-----AFMFLSLPNMLNRPDRKNVKKCSFLKSEFG-----LVWH 187  
 Db 130 TKRGIASLWVIAVVAASVFLVWMDSTNVVSNKAGSNTTRC--FEYERKSKPVLIIH 188  
 QY 188 EIVNYICQVI--FWINFLIVVCTLTITKELYSYVTRGVKVPKKNVKKVFLIIAIVFF 246  
 Db 189 -----ICIVLGFVIFVLLIFCNLVIHTLGRPKVQBNAEV--RRALWVCTVIATV 242  
 QY 247 ICEVPEHFAPIPYTLQSOTRDVFDCTAENTLFVYKSTLWLTSLNACLDPPFYFFICKSFR 306



Db 243 ICFVPHMVQLPWTIAEL-GMPSSNHQAINDAHQVTLCLLSTNCVLDPVVYCLTKKER 301  
Qy 307 NSLISMLKCPNSATSLSDNRKKEQDGGDNEETPM 342  
Db 302 KHLSEKLNIMRSSOKCSRVTTDTGTENAIPIINHVPV 337

Search completed: February 4, 2004, 14:23:34  
Job time : 22 secs

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 4, 2004, 14:22:16 ; Search time 37 Seconds  
(without alignments)  
1935.371 Million cell updates/sec

Title: US-09-780-576-2  
Perfect score: 1778  
Sequence: 1 MQAVNLTSAFGNTSLCTRD.....SQDNKKKQDGDNEETPM 342

Scoring table: BLOSUM62  
Gapop 10.0 , Capext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database : Published Applications AA:

- 1: /cgn2\_6/prodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/prodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/prodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/prodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/prodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/prodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/prodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
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- 10: /cgn2\_6/prodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/prodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
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- 14: /cgn2\_6/prodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/prodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/prodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 17: /cgn2\_6/prodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/prodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1778	100.0	342	9	US-09-835-922-2
2	1778	100.0	342	9	US-09-827-937A-2
3	1778	100.0	342	9	US-09-780-576-2
4	1778	100.0	342	10	US-09-964-008-1
5	1778	100.0	342	12	US-10-272-983-32
6	1778	100.0	342	12	US-09-745-842-6
7	1778	100.0	342	12	US-10-393-807-32
8	1778	100.0	342	12	US-10-417-820A-34
9	1778	100.0	342	15	US-10-225-567A-643
10	1778	100.0	342	15	US-10-333-844-2
11	1748	98.3	342	10	US-09-964-008-3
12	1634	91.9	315	12	US-08-745-842-4
13	1528.5	86.0	343	12	US-09-745-842-2
14	1237.5	69.6	267	12	US-09-745-842-12
15	829	46.6	333	11	US-09-924-125-2

16	829	46.6	333	11	US-09-957-187-2	Sequence 2, Appli
17	829	46.6	333	12	US-10-352-684A-34	Sequence 34, Appli
18	829	46.6	333	12	US-10-308-968-2	Sequence 2, Appli
19	829	46.6	333	15	US-10-243-106-2	Sequence 2, Appli
20	829	46.6	333	15	US-10-189-576-2	Sequence 2, Appli
21	829	46.6	333	15	US-10-225-567A-514	Sequence 514, App
22	823	46.3	333	9	US-09-769-159-2	Sequence 2, Appli
23	823	46.3	333	12	US-10-272-983-18	Sequence 18, Appl
24	823	46.3	333	12	US-10-393-807-18	Sequence 18, Appl
25	823	46.3	333	12	US-10-408-572-2	Sequence 2, Appli
26	823	46.3	333	12	US-10-417-820A-20	Sequence 20, Appli
27	797	44.8	333	9	US-09-848-889-1	Sequence 1, Appli
28	797	44.8	333	12	US-10-100-982-1	Sequence 1, Appli
29	772	43.4	338	15	US-10-024-494-29	Sequence 29, Appl
30	772	43.4	338	10	US-09-919-497-77	Sequence 77, Appl
31	772	43.4	338	12	US-09-745-842-13	Sequence 13, Appl
32	772	43.4	338	12	US-10-352-684A-42	Sequence 42, Appl
33	772	43.4	338	15	US-10-121-101B-10	Sequence 10, Appl
34	772	43.4	338	15	US-10-225-567A-213	Sequence 213, App
35	741.5	41.7	338	9	US-09-826-508-20	Sequence 20, Appl
36	694.5	39.1	358	9	US-09-826-508-10	Sequence 10, Appl
37	694.5	39.1	358	12	US-09-741-783-1	Sequence 1, Appli
38	694.5	39.1	358	12	US-10-295-027-364	Sequence 364, App
39	694.5	39.1	358	12	US-10-295-027-1255	Sequence 1255, Ap
40	694.5	39.1	358	15	US-10-225-567A-418	Sequence 418, App
41	679.5	38.2	358	10	US-09-919-172-22	Sequence 22, Appl
42	679.5	38.2	358	10	US-09-974-298-86	Sequence 86, Appl
43	679.5	38.2	358	15	US-10-121-101B-1	Sequence 1, Appli
44	549.5	30.9	314	12	US-10-264-237-2586	Sequence 2586, Ap
45	546.5	30.7	293	15	US-10-024-494-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1  
US-09-835-922-2  
; Sequence 2, Application US/09835922  
; Patent No. US20010046497A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhang, Fang L.  
; APPLICANT: Luo, Lin  
; APPLICANT: Gustafson, Eric  
; APPLICANT: Liu, Fan-Hui  
; APPLICANT: Chen, Guodong  
; TITLE OF INVENTION: G-Protein Coupled Receptor and Methods  
; FILE REFERENCE: CN01167K  
; CURRENT APPLICATION NUMBER: US/09/835,922  
; CURRENT FILING DATE: 2001-04-16  
; PRIOR APPLICATION NUMBER: US 60/199,041  
; PRIOR FILING DATE: 2000-04-21  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 342  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-09-835-922-2

Query Match 100.0%; Score 1778; DB 9; Length 342;  
Best Local Similarity 100.0%; Pred. No. 8, 1e-159;  
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 MQAVNLTSAFGNTSLCTRDYKIQVLPFLIYTVLFFVGLITNGLAMRIFPQIRSKSNFI 60  
QY 61 IFLKNTVTSLLMLTLPFKILSDAKLGTGPIRTVCQVTSVIFFTWYISISFLGITI 120  
Db 61 IFLKNTVTSLLMLTLPFKILSDAKLGTGPIRTVCQVTSVIFFTWYISISFLGITI 120  
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Db 121 DRYQKTRPFTSNPKNLLGAKILSVVWVWAFMFLSLPNNMLTNRQPRDKNVKVCSEFLKS 180  
Qy 181 EFGLVWHEIVNYICQVIFWFLNFIIVCYTLITKELYRSVYRTRGVGVKVPKKNVNVKFI 240  
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Qy 241 IIAVFFICFVPHFARIPYTLISQTRDVFDCDAENTLFFVKESTLWLTSLNACLDPIFYFF 300  
Db 241 IIAVFFICFVPHFARIPYTLISQTRDVFDCDAENTLFFVKESTLWLTSLNACLDPIFYFF 300  
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Db 301 LCKSFNSLSMLKCPNSATSLSQDNKKKEQDGDPEETPM 342

RESULT 2  
US-09-827-937A-2  
; Sequence 2, Application US/09827937A  
; Patent No. US20020052043A1  
; GENERAL INFORMATION:  
; APPLICANT: Li, Yi  
; APPLICANT: Ruben, Steven M.  
; TITLE OF INVENTION: Human G-Protein Coupled Receptors  
; FILE REFERENCE: 1488.1220003  
; CURRENT APPLICATION NUMBER: US/09/827,937A  
; CURRENT FILING DATE: 2001-04-09  
; PRIOR APPLICATION NUMBER: 08/852,824  
; PRIOR FILING DATE: 1997-05-07  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 342  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-827-937A-2

Query Match 100.0%; Score 1778; DB 9; Length 342;  
Best Local Similarity 100.0%; Pred. No. 8.1e-159;  
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 IFLKNTVISDLMLITPFPKILSDAKLGTGRLTFVQCQVTSVIFFTWYISISFLGLITI 120  
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Qy 241 IIAVFFICFVPHFARIPYTLISQTRDVFDCDAENTLFFVKESTLWLTSLNACLDPIFYFF 300  
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Db 301 LCKSFNSLSMLKCPNSATSLSQDNKKKEQDGDPEETPM 342

RESULT 3  
US-09-780-576-2  
; Sequence 2, Application US/09780576  
; Patent No. US20020072072A1  
; GENERAL INFORMATION:  
; APPLICANT: Civealli, Olivier  
; APPLICANT: No. US20020072072A1hacker, Hans-Peter  
; APPLICANT: Wang, Zhiwei

; APPLICANT: Reinscheid, Rainer  
; TITLE OF INVENTION: ADP-Glucose Receptor  
; FILE REFERENCE: P-UC 4530  
; CURRENT APPLICATION NUMBER: US/09/780,576  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: US 60/234,025  
; PRIOR FILING DATE: 2000-09-20  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 342  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-780-576-2

Query Match 100.0%; Score 1778; DB 9; Length 342;  
Best Local Similarity 100.0%; Pred. No. 8.1e-159;  
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Qy 241 IIAVFFICFVPHFARIPYTLISQTRDVFDCDAENTLFFVKESTLWLTSLNACLDPIFYFF 300  
Db 241 IIAVFFICFVPHFARIPYTLISQTRDVFDCDAENTLFFVKESTLWLTSLNACLDPIFYFF 300  
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Db 301 LCKSFNSLSMLKCPNSATSLSQDNKKKEQDGDPEETPM 342

RESULT 4  
US-09-964-008-1  
; Sequence 1, Application US/09964008  
; Patent No. US20020156246A1  
; GENERAL INFORMATION:  
; APPLICANT: Glucksmann, Maria A.  
; APPLICANT: Gu, Wei  
; TITLE OF INVENTION: 15625 Receptor, A No. US20020156246A1e1 G-Protein Coupled Recept  
; FILE REFERENCE: 5800-13, 035800-171548  
; CURRENT APPLICATION NUMBER: US/09/964,008  
; CURRENT FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: 09/187,134  
; PRIOR FILING DATE: 1998-11-06  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 342  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-964-008-1

Query Match 100.0%; Score 1778; DB 10; Length 342;  
Best Local Similarity 100.0%; Pred. No. 8.1e-159;  
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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## RESULT 5

US-10-272-983-32  
; Sequence 32, Application US/10272983  
; Publication No. US20030148450A1  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Dang, Huong T.  
; APPLICANT: Liaw, Chen W.  
; APPLICANT: Lin, I-Lin  
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors  
; FILE REFERENCE: AREN0050  
; CURRENT APPLICATION NUMBER: US/10/272,983  
; PRIOR FILING DATE: 2002-10-17  
; PRIOR APPLICATION NUMBER: US/09/417,044  
; PRIOR FILING DATE: 1999-10-12  
; PRIOR APPLICATION NUMBER: 60/109,213  
; PRIOR FILING DATE: 1998-11-20  
; PRIOR APPLICATION NUMBER: 60/120,416  
; PRIOR FILING DATE: 1999-02-16  
; PRIOR APPLICATION NUMBER: 60/121,851  
; PRIOR FILING DATE: 1999-02-26  
; PRIOR APPLICATION NUMBER: 60/123,946  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,949  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/136,436  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/136,437  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/136,439  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/136,567  
; PRIOR FILING DATE: 1999-05-28  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 32  
; LENGTH: 342  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-272-983-32

Query Match 100.0%; Score 1778; DB 12; Length 342;  
Best Local Similarity 100.0%; Pred. No. 8.1e-159;  
Matches 342; Conservative 0; Mismatches -0; Indels 0; Gaps 0;

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DB 61 IFLKNTVISDLLMLTFFPKILSDAKLGTGRLTFCVQVTSVIFFTMYISISFLGLITI 120  
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QY 181 EFGVLWHEIWNVICQVIFWFLNFIIVCVTLITKELYRSYVTRGVGVKPRKKNVKVFI 240  
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QY 241 IIAVFFICFVPPHARIPYTLSTQTRVDFDCTAENTLFFYVKESTLMTSLNACLDPIYFF 300  
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QY 301 LCKSFRNSLSMLKCPNSATSLSDNRKKEQDGDNEETPM 342  
DB 301 LCKSFRNSLSMLKCPNSATSLSDNRKKEQDGDNEETPM 342

## RESULT 6

US-09-745-842-6  
; Sequence 6, Application US/09745842  
; Publication No. US20030170777A1  
; GENERAL INFORMATION:  
; APPLICANT: Conley, Pamela B.  
; APPLICANT: Jantzen, Hans-Michael  
; APPLICANT: Ramakrishnan-DuBridge, Vanitha  
; APPLICANT: Julius, David  
; APPLICANT: Hollopetter, Gunter  
; APPLICANT: COR Therapeutics, Inc.  
; TITLE OF INVENTION: P2Y12 Receptor  
; FILE REFERENCE: 44481-5053-US  
; CURRENT APPLICATION NUMBER: US/09/745,842  
; PRIOR FILING DATE: 2000-12-26  
; PRIOR APPLICATION NUMBER: US 60/171,622  
; PRIOR FILING DATE: 1999-12-23  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 342  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-745-842-6

Query Match 100.0%; Score 1778; DB 12; Length 342;  
Best Local Similarity 100.0%; Pred. No. 8.1e-159;  
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MQAVDNLTSAAGNTSLCTRDYKIQVLPFLLYTVLPVGLITNGLAMRIFPQIRSKSNFI 60  
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DB 61 IFLKNTVISDLLMLTFFPKILSDAKLGTGRLTFCVQVTSVIFFTMYISISFLGLITI 120  
QY 121 DRYOKTTRPFTSNPKNLLGAKILSVVIWAFMFLSLPNMILTNQPRDKNVKCSFLKS 180  
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QY 241 IIAVFFICFVPPHARIPYTLSTQTRVDFDCTAENTLFFYVKESTLMTSLNACLDPIYFF 300  
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DB 301 LCKSFRNSLSMLKCPNSATSLSDNRKKEQDGDNEETPM 342

RESULT 7  
US-10-393-807-32  
; Sequence 32, Application US/10393807  
; Publication No. US20030175891A1  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Dang, Huong T.  
; APPLICANT: Liaw, Chen W.  
; APPLICANT: Lin, I-Lin  
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors  
; FILE REFERENCE: AREN0050  
; CURRENT APPLICATION NUMBER: US/10/393,807  
; CURRENT FILING DATE: 2003-03-21  
; PRIOR APPLICATION NUMBER: US/09/417,044  
; PRIOR FILING DATE: 1999-10-12  
; PRIOR APPLICATION NUMBER: 60/109,213  
; PRIOR FILING DATE: 1998-11-20  
; PRIOR APPLICATION NUMBER: 60/120,416  
; PRIOR FILING DATE: 1999-02-16  
; PRIOR APPLICATION NUMBER: 60/121,851  
; PRIOR FILING DATE: 1999-02-26  
; PRIOR APPLICATION NUMBER: 60/123,946  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,949  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/136,436  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/136,437  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/136,439  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/136,567  
; PRIOR FILING DATE: 1999-05-28  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 32  
; LENGTH: 342  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-393-807-32

Query Match 100.0%; Score 1778; DB 12; Length 342;  
Best Local Similarity 100.0%; Pred. No. 8.1e-159;  
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQAVNLTSPAGNTSLCTRDYKITQVLPFLYTVLFFVGLITNGLAMRIFPQIRSKSNFI 60  
DB 1 MQAVNLTSPAGNTSLCTRDYKITQVLPFLYTVLFFVGLITNGLAMRIFPQIRSKSNFI 60  
QY 61 IFLKNTVISDLLMILTPFPKILSDAKLGTGPLRTFVCQVTSVIFFTWYISISFLGLITI 120  
DB 61 IFLKNTVISDLLMILTPFPKILSDAKLGTGPLRTFVCQVTSVIFFTWYISISFLGLITI 120  
QY 121 DRYQKTRFPKTSNPKNLGAKILSVIWAEMFLLSLPNMILTNRPDKXKVKCSFLKS 180  
DB 121 DRYQKTRFPKTSNPKNLGAKILSVIWAEMFLLSLPNMILTNRPDKXKVKCSFLKS 180  
QY 181 EFLGVWHEIWNVICQVIFWINEFLIVVCYTLITKELYSYVTRGVGVPRKKNVKVFI 240  
DB 181 EFLGVWHEIWNVICQVIFWINEFLIVVCYTLITKELYSYVTRGVGVPRKKNVKVFI 240  
QY 241 IIAVFFICVPPHFARIPTVLTQTRDVFCDTAENTLFVYKESTLWLTSLNACLDPFYIFF 300  
DB 241 IIAVFFICVPPHFARIPTVLTQTRDVFCDTAENTLFVYKESTLWLTSLNACLDPFYIFF 300  
QY 301 LCKSPFNLSIIMLKCPSNATSLSQDNKKEQDGGDPNEETPM 342  
DB 301 LCKSPFNLSIIMLKCPSNATSLSQDNKKEQDGGDPNEETPM 342

Sequence 34, Application US/10417820A  
; Publication No. US20030229216A1  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Liaw, Chen W.  
; APPLICANT: Lowitz, Kevin  
; APPLICANT: Chalmers, Derek T.  
; APPLICANT: Behan, Dominic P.  
; TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled  
; TITLE OF INVENTION: Receptors  
; FILE REFERENCE: 7.US28.CON  
; CURRENT APPLICATION NUMBER: US/10/417,820A  
; CURRENT FILING DATE: 2003-04-16  
; PRIOR APPLICATION NUMBER: 09/416,760  
; PRIOR FILING DATE: 1999-10-12  
; PRIOR APPLICATION NUMBER: 09/170,496  
; PRIOR FILING DATE: 1998-10-13  
; PRIOR APPLICATION NUMBER: 60/110,060  
; PRIOR FILING DATE: 1998-11-27  
; PRIOR APPLICATION NUMBER: 60/120,416  
; PRIOR FILING DATE: 1999-02-16  
; PRIOR APPLICATION NUMBER: 60/121,852  
; PRIOR FILING DATE: 1999-02-26  
; PRIOR APPLICATION NUMBER: 60/109,213  
; PRIOR FILING DATE: 1998-11-20  
; PRIOR APPLICATION NUMBER: 60/123,944  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,945  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,948  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,951  
; PRIOR FILING DATE: 1999-03-12  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 155  
; SOFTWARE: Patent In version 3.2  
; SEQ ID NO 34  
; LENGTH: 342  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-417-820A-34

Query Match 100.0%; Score 1778; DB 12; Length 342;  
Best Local Similarity 100.0%; Pred. No. 8.1e-159;  
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQAVNLTSPAGNTSLCTRDYKITQVLPFLYTVLFFVGLITNGLAMRIFPQIRSKSNFI 60  
DB 1 MQAVNLTSPAGNTSLCTRDYKITQVLPFLYTVLFFVGLITNGLAMRIFPQIRSKSNFI 60  
QY 61 IFLKNTVISDLLMILTPFPKILSDAKLGTGPLRTFVCQVTSVIFFTWYISISFLGLITI 120  
DB 61 IFLKNTVISDLLMILTPFPKILSDAKLGTGPLRTFVCQVTSVIFFTWYISISFLGLITI 120  
QY 121 DRYQKTRFPKTSNPKNLGAKILSVIWAEMFLLSLPNMILTNRPDKXKVKCSFLKS 180  
DB 121 DRYQKTRFPKTSNPKNLGAKILSVIWAEMFLLSLPNMILTNRPDKXKVKCSFLKS 180  
QY 181 EFLGVWHEIWNVICQVIFWINEFLIVVCYTLITKELYSYVTRGVGVPRKKNVKVFI 240  
DB 181 EFLGVWHEIWNVICQVIFWINEFLIVVCYTLITKELYSYVTRGVGVPRKKNVKVFI 240  
QY 241 IIAVFFICVPPHFARIPTVLTQTRDVFCDTAENTLFVYKESTLWLTSLNACLDPFYIFF 300  
DB 241 IIAVFFICVPPHFARIPTVLTQTRDVFCDTAENTLFVYKESTLWLTSLNACLDPFYIFF 300  
QY 301 LCKSPFNLSIIMLKCPSNATSLSQDNKKEQDGGDPNEETPM 342  
DB 301 LCKSPFNLSIIMLKCPSNATSLSQDNKKEQDGGDPNEETPM 342

; Sequence 643, Application US/10225567A

; Publication No. US20030113798A1

; GENERAL INFORMATION:

; APPLICANT: Lifespan Biosciences

; APPLICANT: Brown, Joseph P.

; APPLICANT: Burmer, Glenna C.

; APPLICANT: Roush, Christine L.

; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS

; FILE REFERENCE: 1920-4-4

; CURRENT APPLICATION NUMBER: US/10/225,567A

; CURRENT FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 60/257,144

; PRIOR FILING DATE: 2000-12-19

; NUMBER OF SEQ ID NOS: 2292

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 643

; LENGTH: 342

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-225-567A-643

Query Match 100.0%; Score 1778; DB 15; Length 342;

Best Local Similarity 100.0%; Pred. No. 8.1e-159;

Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQAVDNLTSAPGNTSLCTRDYKIQVLPFLYTVLFFVGLITNGLAMRIPFQIRSKSNFI 60

DB 1 MQAVDNLTSAPGNTSLCTRDYKIQVLPFLYTVLFFVGLITNGLAMRIPFQIRSKSNFI 60

QY 61 IFLKNTVISDLMLITPPFKILSDAKLGTGRLTFVFCQVTSVIFFTMYISISFLGLITI 120

DB 61 IFLKNTVISDLMLITPPFKILSDAKLGTGRLTFVFCQVTSVIFFTMYISISFLGLITI 120

QY 121 DRYQKTRPPFKTSNPKNLLGAKILSVIWAFFLLSLPNMILNRPDRDNKVKCSFLKS 180

DB 121 DRYQKTRPPFKTSNPKNLLGAKILSVIWAFFLLSLPNMILNRPDRDNKVKCSFLKS 180

QY 181 EFGLVWHEIVNYICQVIFWIFNLIVCYTLITKELYSYVTRGVGVKPKKVNKVF 240

DB 181 EFGLVWHEIVNYICQVIFWIFNLIVCYTLITKELYSYVTRGVGVKPKKVNKVF 240

QY 241 IIAVFFICFVFPFHARIPYTLISQTRDVFDCVTAENTLFYVKESTLWLTSLNACLDPIFYFF 300

DB 241 IIAVFFICFVFPFHARIPYTLISQTRDVFDCVTAENTLFYVKESTLWLTSLNACLDPIFYFF 300

QY 301 LCKSPRNSLSMLKCPNSATSLSQDNRRKKEQDGGDPNEETPM 342

DB 301 LCKSPRNSLSMLKCPNSATSLSQDNRRKKEQDGGDPNEETPM 342

RESULT 10

US-10-333-844-2

; Sequence 2, Application US/10333944

; Publication No. US20030124626A1

; GENERAL INFORMATION:

; APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.

; TITLE OF INVENTION: Method for screening antiplatelet agents

; FILE REFERENCE: Y0122PCT-656

; CURRENT APPLICATION NUMBER: US/10/333,844

; CURRENT FILING DATE: 2003-01-24

; PRIOR APPLICATION NUMBER: JP 2000-334721

; PRIOR FILING DATE: 2000-11-01

; PRIOR APPLICATION NUMBER: JP 2001-3577

; PRIOR FILING DATE: 2001-01-11

; NUMBER OF SEQ ID NOS: 12

; SEQ ID NO 2

; LENGTH: 342

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-333-844-2

Query Match 100.0%; Score 1778; DB 15; Length 342;

Best Local Similarity 100.0%; Pred. No. 8.1e-159;

Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQAVDNLTSAPGNTSLCTRDYKIQVLPFLYTVLFFVGLITNGLAMRIPFQIRSKSNFI 60

DB 1 MQAVDNLTSAPGNTSLCTRDYKIQVLPFLYTVLFFVGLITNGLAMRIPFQIRSKSNFI 60

QY 61 IFLKNTVISDLMLITPPFKILSDAKLGTGRLTFVFCQVTSVIFFTMYISISFLGLITI 120

DB 61 IFLKNTVISDLMLITPPFKILSDAKLGTGRLTFVFCQVTSVIFFTMYISISFLGLITI 120

QY 121 DRYQKTRPPFKTSNPKNLLGAKILSVIWAFFLLSLPNMILNRPDRDNKVKCSFLKS 180

DB 121 DRYQKTRPPFKTSNPKNLLGAKILSVIWAFFLLSLPNMILNRPDRDNKVKCSFLKS 180

QY 181 EFGLVWHEIVNYICQVIFWIFNLIVCYTLITKELYSYVTRGVGVKPKKVNKVF 240

DB 181 EFGLVWHEIVNYICQVIFWIFNLIVCYTLITKELYSYVTRGVGVKPKKVNKVF 240

QY 241 IIAVFFICFVFPFHARIPYTLISQTRDVFDCVTAENTLFYVKESTLWLTSLNACLDPIFYFF 300

DB 241 IIAVFFICFVFPFHARIPYTLISQTRDVFDCVTAENTLFYVKESTLWLTSLNACLDPIFYFF 300

Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQAVDNLTSAPGNTSLCTRDYKIQVLPFLYTVLFFVGLITNGLAMRIPFQIRSKSNFI 60

DB 1 MQAVDNLTSAPGNTSLCTRDYKIQVLPFLYTVLFFVGLITNGLAMRIPFQIRSKSNFI 60

QY 61 IFLKNTVISDLMLITPPFKILSDAKLGTGRLTFVFCQVTSVIFFTMYISISFLGLITI 120

DB 61 IFLKNTVISDLMLITPPFKILSDAKLGTGRLTFVFCQVTSVIFFTMYISISFLGLITI 120

QY 121 DRYQKTRPPFKTSNPKNLLGAKILSVIWAFFLLSLPNMILNRPDRDNKVKCSFLKS 180

DB 121 DRYQKTRPPFKTSNPKNLLGAKILSVIWAFFLLSLPNMILNRPDRDNKVKCSFLKS 180

QY 181 EFGLVWHEIVNYICQVIFWIFNLIVCYTLITKELYSYVTRGVGVKPKKVNKVF 240

DB 181 EFGLVWHEIVNYICQVIFWIFNLIVCYTLITKELYSYVTRGVGVKPKKVNKVF 240

QY 241 IIAVFFICFVFPFHARIPYTLISQTRDVFDCVTAENTLFYVKESTLWLTSLNACLDPIFYFF 300

DB 241 IIAVFFICFVFPFHARIPYTLISQTRDVFDCVTAENTLFYVKESTLWLTSLNACLDPIFYFF 300

QY 301 LCKSPRNSLSMLKCPNSATSLSQDNRRKKEQDGGDPNEETPM 342

DB 301 LCKSPRNSLSMLKCPNSATSLSQDNRRKKEQDGGDPNEETPM 342

RESULT 11

US-09-964-008-3

; Sequence 3, Application US/09964008

; Patent No. US20020156246A1

; GENERAL INFORMATION:

; APPLICANT: Glucksmann, Maria A.

; APPLICANT: Gu, Wei

; TITLE OF INVENTION: 15625 Receptor, A No. US20020156246A1

; FILE REFERENCE: 5800-13, 035800-171548

; CURRENT APPLICATION NUMBER: US/09/964,008

; CURRENT FILING DATE: 2001-09-26

; PRIOR APPLICATION NUMBER: 09/187,134

; PRIOR FILING DATE: 1998-11-06

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 3

; LENGTH: 342

; TYPE: PRT

; ORGANISM: Macaca sp.

US-09-964-008-3

Query Match 98.3%; Score 1748; DB 10; Length 342;

Best Local Similarity 98.0%; Pred. No. 5.3e-156;

Matches 335; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MQAVDNLTSAPGNTSLCTRDYKIQVLPFLYTVLFFVGLITNGLAMRIPFQIRSKSNFI 60

DB 1 MQAVDNLTSAPGNTSLCTRDYKIQVLPFLYTVLFFVGLITNGLAMRIPFQIRSKSNFI 60

QY 61 IFLKNTVISDLMLITPPFKILSDAKLGTGRLTFVFCQVTSVIFFTMYISISFLGLITI 120

DB 61 IFLKNTVISDLMLITPPFKILSDAKLGTGRLTFVFCQVTSVIFFTMYISISFLGLITI 120

QY 121 DRYQKTRPPFKTSNPKNLLGAKILSVIWAFFLLSLPNMILNRPDRDNKVKCSFLKS 180

DB 121 DRYQKTRPPFKTSNPKNLLGAKILSVIWAFFLLSLPNMILNRPDRDNKVKCSFLKS 180

QY 181 EFGLVWHEIVNYICQVIFWIFNLIVCYTLITKELYSYVTRGVGVKPKKVNKVF 240

DB 181 EFGLVWHEIVNYICQVIFWIFNLIVCYTLITKELYSYVTRGVGVKPKKVNKVF 240

QY 241 IIAVFFICFVFPFHARIPYTLISQTRDVFDCVTAENTLFYVKESTLWLTSLNACLDPIFYFF 300

DB 241 IIAVFFICFVFPFHARIPYTLISQTRDVFDCVTAENTLFYVKESTLWLTSLNACLDPIFYFF 300

QY 301 LCKSPRNSLSMLKCPNSATSLSQDNRRKKEQDGGDPNEETPM 342

Db 301 LCKGFRNLSMLKCPNSATSQSDNRKKBQDGGDPNEETPM 342

RESULT 12

US-09-745-842-4  
 ; Sequence 4, Application US/09745842  
 ; Publication No. US2003017077A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Conley, Pamela B.  
 ; APPLICANT: Jantzen, Hans-Michael  
 ; APPLICANT: Ramakrishnan-Dubridge, Vanitha  
 ; APPLICANT: Julius, David  
 ; APPLICANT: Hollopeter, Gunter  
 ; APPLICANT: COR Therapeutics, Inc.  
 ; TITLE OF INVENTION: F2Y12 Receptor  
 ; FILE REFERENCE: 44481-5053-US  
 ; CURRENT APPLICATION NUMBER: US/09/745,842  
 ; CURRENT FILING DATE: 2000-12-26  
 ; PRIOR APPLICATION NUMBER: US 60/171,622  
 ; PRIOR FILING DATE: 1999-12-23  
 ; NUMBER OF SEQ ID NOS: 21  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 4  
 ; LENGTH: 315  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-745-842-4

Query Match 91.9%; Score 1634; DB 12; Length 315;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-145;  
 Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MOAVDNLTSAPGNTSLCTRDYKTIQVLPFLYTVLFFVGLITNGLAMRIFFOIRSKSNFI 60  
 Db 1 MOAVDNLTSAPGNTSLCTRDYKTIQVLPFLYTVLFFVGLITNGLAMRIFFOIRSKSNFI 60  
 QY 61 IFLKNTVISDLMLTPFPFKILSDAKLTGTPRTFVQVTSVIFFTMYISIFLGLITI 120  
 Db 61 IFLKNTVISDLMLTPFPFKILSDAKLTGTPRTFVQVTSVIFFTMYISIFLGLITI 120  
 QY 121 DRYQKTPPTSPKPNKLLGAKILSVIWAFFMLSLPNMILTNRPDKNVKKSFLKS 180  
 Db 121 DRYQKTPPTSPKPNKLLGAKILSVIWAFFMLSLPNMILTNRPDKNVKKSFLKS 180  
 QY 181 BFLGVWHEIVNYICQVIFWIFNLIVCYTLITKELYRSYVTRGVKVPKKNVKVFI 240  
 Db 181 BFLGVWHEIVNYICQVIFWIFNLIVCYTLITKELYRSYVTRGVKVPKKNVKVFI 240  
 QY 241 IIAVFFICFVPHFARIPTLSQTRDVEDCTAENTLFYVKESTLWLSNACLDPPFIYFF 300  
 Db 241 IIAVFFICFVPHFARIPTLSQTRDVEDCTAENTLFYVKESTLWLSNACLDPPFIYFF 300  
 QY 301 LCKSPRNSLSMLKC 315  
 Db 301 LCKSPRNSLSMLKC 315

RESULT 13

US-09-745-842-2  
 ; Sequence 2, Application US/09745842  
 ; Publication No. US2003017077A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Conley, Pamela B.  
 ; APPLICANT: Jantzen, Hans-Michael  
 ; APPLICANT: Ramakrishnan-Dubridge, Vanitha  
 ; APPLICANT: Julius, David  
 ; APPLICANT: Hollopeter, Gunter  
 ; APPLICANT: COR Therapeutics, Inc.  
 ; TITLE OF INVENTION: F2Y12 Receptor  
 ; FILE REFERENCE: 44481-5053-US  
 ; CURRENT APPLICATION NUMBER: US/09/745,842  
 ; CURRENT FILING DATE: 2000-12-26

; PRIOR APPLICATION NUMBER: US 60/171,622  
 ; PRIOR FILING DATE: 1999-12-23  
 ; NUMBER OF SEQ ID NOS: 21  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 2  
 ; LENGTH: 343  
 ; TYPE: PRT  
 ; ORGANISM: Rattus norvegicus  
 US-09-745-842-2  
 Query Match 86.0%; Score 1528.5; DB 12; Length 343;  
 Best Local Similarity 86.9%; Pred. No. 2.2e-135;  
 Matches 293; Conservative 17; Mismatches 22; Indels 5; Gaps 1;  
 QY 6 NLTSAPGNTSLCTRDYKTIQVLPFLYTVLFFVGLITNGLAMRIFFOIRSKSNFIILKN 65  
 Db 12 NLTSAPGNTSLCTRDYKTIQVLPFLYTVLFFVGLITNGLAMRIFFOIRSKSNFIILKN 71  
 QY 66 TVISDLMLTPFPFKILSDAKLTGTPRTFVQVTSVIFFTMYISIFLGLITIDRYK 125  
 Db 72 TVISDLMLTPFPFKILSDAKLTGTPRTFVQVTSVIFFTMYISIFLGLITIDRYK 131  
 QY 126 TTRPKTSNPNKLLGAKILSVIWAFFMLSLPNMILTNRPDKNVKKSFLKSEGLV 185  
 Db 132 TTRPKTSNPNKLLGAKILSVIWAFFMLSLPNMILTNRPDKNVKKSFLKSEGLV 191  
 QY 186 WHEIVNYICQVIFWIFNLIVCYTLITKELYRSYVTRGVKVPKKNVKVFIILAVF 245  
 Db 192 WHEIVNYICQVIFWIFNLIVCYTLITKELYRSYVTRGVKVPKKNVKVFIILAVF 251  
 QY 246 FICFVPHFARIPTLSQTRDVEDCTAENTLFYVKESTLWLSNACLDPPFIYFLCKSF 305  
 Db 252 FICFVPHFARIPTLSQTRDVEDCTAENTLFYVKESTLWLSNACLDPPFIYFLCKSF 311  
 QY 306 RNSLSMLKCPNSATSLSQDNRKKEQDGGDPNEETPM 342  
 Db 312 RNSLSMLKCPNSATSLSQDNRKKEQDGGDPNEETPM 343

RESULT 14

US-09-745-842-12  
 ; Sequence 12, Application US/09745842  
 ; Publication No. US2003017077A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Conley, Pamela B.  
 ; APPLICANT: Jantzen, Hans-Michael  
 ; APPLICANT: Ramakrishnan-Dubridge, Vanitha  
 ; APPLICANT: Julius, David  
 ; APPLICANT: Hollopeter, Gunter  
 ; APPLICANT: COR Therapeutics, Inc.  
 ; TITLE OF INVENTION: F2Y12 Receptor  
 ; FILE REFERENCE: 44481-5053-US  
 ; CURRENT APPLICATION NUMBER: US/09/745,842  
 ; CURRENT FILING DATE: 2000-12-26  
 ; PRIOR APPLICATION NUMBER: US 60/171,622  
 ; PRIOR FILING DATE: 1999-12-23  
 ; NUMBER OF SEQ ID NOS: 21  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 12  
 ; LENGTH: 267  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-745-842-12

Query Match 69.6%; Score 1237.5; DB 12; Length 267;  
 Best Local Similarity 95.7%; Pred. No. 3.5e-108;  
 Matches 242; Conservative 3; Mismatches 7; Indels 1; Gaps 1;  
 QY 1 MOAVDNLTSAPGNTSLCTRDYKTIQVLPFLYTVLFFVGLITNGLAMRIFFOIRSKSNFI 60  
 Db 1 MOAVDNLTSAPGNTSLCTRDYKTIQVLPFLYTVLFFVGLITNGLAMRIFFOIRSKSNFI 60  
 QY 61 IFLKNTVISDLMLTPFPFKILSDAKLTGTPRTFVQVTSVIFFTMYISIFLGLITI 120



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Db 61 IFLNNTVISDLLMLTTPFKILSDAKLGTGLRTFVCQVTSVIFYFTMYISFLGLITI 120
Qy 121 DRYOKTRPRKTSNPKNLLGAKILSVVIAFMFLLSLPNMILNROPRDKNVKCSFLKS 180
Db 121 DRYOKTRPRKTSNPKNLLGAKILSVVIAFMFLLSLPNMILNROPRDKNVKCSFLKS 180
Qy 181 EFGLVWHEIVNYICQVIFWNLFLIVICYTLITKELYRSVVRTRGVGKVPKKNVKVFI 240
Db 181 EFGLVWHEIVNYICQVIFWNLFLIVICYTLITKELYRSVVRTRGVGKVPKKNVKVFI 240
Qy 241 IIAVFFI-CFVPF 252
Db 241 HCCILYLFCSPPF 253
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## RESULT 15

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US-09-924-125-2
; Sequence 2, Application US/09924125
; Publication No. US20030050235A1
; GENERAL INFORMATION:
; APPLICANT: Communi, Didier
; TITLE OF INVENTION: THE NATURAL LIGAND FOR ORPHAN G PROTEIN COUPLED RECEPTOR GPR86 AN
; FILE REFERENCE: 9049/2092
; CURRENT APPLICATION NUMBER: US/09/924,125
; CURRENT FILING DATE: 2001-07-08
; PRIOR APPLICATION NUMBER: US 09/924,125
; PRIOR FILING DATE: 2001-07-08
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-924-125-2
```

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Query Match 46.68; Score 829; DB 11; Length 333;
Best Local Similarity 49.18; Pred.No.1.le-69;
Matches 155; Conservative 57; Mismatches 102; Indels 2; Gaps 1;

Qy 17 CTRDYKITQVLPPLLYTVLFFVGLITNGLAMRIFFQIRSKSNFIIFLKNTVISDLMILT 76
Db 15 CPDRTRIVQLVFPALYTVVFLTGILLNTLALWVFIIPSSSTFIYLYKNTLVADLIMTLM 74
Qy 77 FPFKILSDAKLGTGLRTFVCQVTSVIFYFTMYISFLGLITIDRYOKTRPRKTSNEK 136
Db 75 LPFKILSDSHLAPQLRAFVCRFSSVIFYETMYVGVILLGLIAFDRLKIIRPLRNIFLK 134
Qy 137 NLLGAKILSVVIAFMFLLSLPNMILNROPRDKNVKCSFLKSEFGLVWHEIVNYICQV 196
Db 135 KPVEAKTVSIFWFFLFISLPNNILSNKEATPSSVKCSKASLGLGLKWHQVNNICQF 194
Qy 197 IFWNLFLIVICYTLITKELYRSVVRTRGVGKVPKKNVKVFIIAVFFICFVPFHPAR 256
Db 195 IFWTVFILMLVYVYVIAKVYDYSYRSKSKDRKNKKGKGVVAVFVCFVCFHPAR 254
Qy 257 IPYTLSDTRDVFDCVTAENTLFFVKESTLWLTSLNACLDPIYFPFLCKSPRNSLSMLKCP 316
Db 255 VPYTHSQTNKTKDRLQNLQFIKAKETTLFLAANNICMDPLIYIFLCKKTEKLPCCNQ-G 312
Qy 317 NSATSLSDQNRKKEQD 332
Db 313 RKTASSQENHSQTD 328
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Search completed: February 4, 2004, 14:28:07  
Job time : 38 secs





Db 1 MQAVDNLTSAAGNTSLCTRDYKITQVLFPLLYTVLFPVGLITNGLAMRIFFQIRSKSNFI 60  
QY 61 IFLKNTVISDLLMLTPFPKILSDAKLGTGTLRTFVCQVTSVIFFTMYISISFLGLITI 120  
Db 61 IFLKNTVISDLLMLTPFPKILSDAKLGTGTLRTFVCQVTSVIFFTMYISISFLGLITI 120  
QY 121 DRYQKTRPPKTSNPKNLLGAKILSVVIWAFMFLSLPNMILTNRQPRDKNVKCSFLKS 180  
Db 121 DRYQKTRPPKTSNPKNLLGAKILSVVIWAFMFLSLPNMILTNRQPRDKNVKCSFLKS 180  
QY 181 EFGLVWHEIYVNYICQVIFWNLFLIVCYTLITKELYRSYVTRGVGKVPKKNVKVFI 240  
Db 181 EFGLVWHEIYVNYICQVIFWNLFLIVCYTLITKELYRSYVTRGVGKVPKKNVKVFI 240  
QY 241 IIAVFFICFVFPFHARIPYTLSTQTRDVFDCQVTSVIFFTMYISISFLGLITI 300  
Db 241 IIAVFFICFVFPFHARIPYTLSTQTRDVFDCQVTSVIFFTMYISISFLGLITI 300  
QY 301 LCKSFRNSLISMLKCPNSATSLSDNRKKEQDGDGDPNEETPM 342  
Db 301 LCKSFRNSLISMLKCPNSATSLSDNRKKEQDGDGDPNEETPM 342

RESULT 3  
ID AAB02840  
XX AAB02840 standard; Protein; 342 AA.  
AC AAB02840;  
XX 22-AUG-2000 (first entry)  
DT Human G protein coupled receptor hchn8 protein SEQ ID NO:34.  
DE Human; G protein coupled receptor; GPCR; transmembrane receptor;  
KW identification; agonist; screening; therapeutic; pharmaceutical;  
KW mutant.  
XX Homo sapiens.  
OS WO200022131-A2.  
EN 20-APR-2000.  
PD 13-OCT-1999; 99WO-US24065.  
PF 13-OCT-1998; 98US-0170496.  
PR 12-NOV-1998; 98US-0108029.  
PR 20-NOV-1998; 98US-0109213.  
PR 27-NOV-1998; 98US-0110060.  
PR 16-FEB-1999; 99US-0120416.  
PR 26-FEB-1999; 99US-0121852.  
PR 12-MAR-1999; 99US-0123944.  
PR 12-MAR-1999; 99US-0123945.  
PR 12-MAR-1999; 99US-0123946.  
PR 12-MAR-1999; 99US-0123948.  
PR 12-MAR-1999; 99US-0123949.  
PR 12-MAR-1999; 99US-0123951.  
PR 28-MAY-1999; 99US-0136436.  
PR 28-MAY-1999; 99US-0136437.  
PR 28-MAY-1999; 99US-0136439.  
PR 28-MAY-1999; 99US-0137127.  
PR 28-MAY-1999; 99US-0137131.  
PR 28-MAY-1999; 99US-0137567.  
PR 30-JUN-1999; 99US-0141448.  
PR 27-AUG-1999; 99US-0151114.  
PR 03-SEP-1999; 99US-0152524.  
PR 29-SEP-1999; 99US-0156633.  
PR 29-SEP-1999; 99US-0156634.  
PR 29-SEP-1999; 99US-0156634.  
XX (AREN-) ARENA PHARM INC.  
PA Behan DP, Lehmann-Bruinsma K, Chalmers DT, Chen R, Dang HT;  
XX

Gore M, Liaw CW, Lin I, Lowitz K, White C;  
XX WPI; 2000-317986/27.  
DR N-PSDB; AAA46034.  
XX Non-endogenous, human G protein-coupled receptors for screening  
PT receptor, inverse of partial agonists useful as therapeutic agents -  
XX Example 1; Page 112-113; 187pp; English.  
XX The present invention describes transmembrane receptors, preferably  
CC human G protein coupled receptors (GPCR), for which the endogenous  
CC ligand is unknown (orphan GPCR receptors). More specifically the present  
CC invention relates to non-endogenous, constitutively activated versions  
CC of a human GPCR. These non-endogenous human GPCRs can be useful for  
CC the direct identification of candidate compounds as receptors agonists,  
CC inverse agonists or partial agonists for use as pharmaceutical agents.  
CC AAA46017 to AAA46126 and AAB02825 to AAB02859 represent sequences used in  
CC the exemplification of the present invention.  
XX Sequence 342 AA;  
SQ Query Match 100.0%; Score 1778; DB 21; Length 342;  
Best Local Similarity 100.0%; Pred. No. 5.3e-187;  
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MQAVDNLTSAAGNTSLCTRDYKITQVLFPLLYTVLFPVGLITNGLAMRIFFQIRSKSNFI 60  
Db 1 MQAVDNLTSAAGNTSLCTRDYKITQVLFPLLYTVLFPVGLITNGLAMRIFFQIRSKSNFI 60  
QY 61 IFLKNTVISDLLMLTPFPKILSDAKLGTGTLRTFVCQVTSVIFFTMYISISFLGLITI 120  
Db 61 IFLKNTVISDLLMLTPFPKILSDAKLGTGTLRTFVCQVTSVIFFTMYISISFLGLITI 120  
QY 121 DRYQKTRPPKTSNPKNLLGAKILSVVIWAFMFLSLPNMILTNRQPRDKNVKCSFLKS 180  
Db 121 DRYQKTRPPKTSNPKNLLGAKILSVVIWAFMFLSLPNMILTNRQPRDKNVKCSFLKS 180  
QY 181 EFGLVWHEIYVNYICQVIFWNLFLIVCYTLITKELYRSYVTRGVGKVPKKNVKVFI 240  
Db 181 EFGLVWHEIYVNYICQVIFWNLFLIVCYTLITKELYRSYVTRGVGKVPKKNVKVFI 240  
QY 241 IIAVFFICFVFPFHARIPYTLSTQTRDVFDCQVTSVIFFTMYISISFLGLITI 300  
Db 241 IIAVFFICFVFPFHARIPYTLSTQTRDVFDCQVTSVIFFTMYISISFLGLITI 300  
QY 301 LCKSFRNSLISMLKCPNSATSLSDNRKKEQDGDGDPNEETPM 342  
Db 301 LCKSFRNSLISMLKCPNSATSLSDNRKKEQDGDGDPNEETPM 342  
RESULT 4  
ID AAY94444  
XX AAY94444 standard; protein; 342 AA.  
AC AAY94444;  
XX 21-AUG-2000 (first entry)  
DT Human 15625 receptor protein.  
DE Human; G-protein-coupled receptor; GPCR; 15625 receptor protein;  
KW Gliol cells; spleen; colon; liver; brain; T-cell; heart; 3;  
KW red cell; thymus; B-cell; pancreas; disorder; chromosome 3;  
KW anaemia; neutropenia; thrombocytopenia; gene therapy; 88.  
OS Homo sapiens.  
XX Location/Qualifiers  
FH Key 1..25  
FT Domain /label= extracellular\_domain  
FT Modified-site 6..9  
FT /label= N-glycosylation

FT Misc-difference 13 /note= "encoded by ACC"  
FT Modified-site 13..16  
FT Domain 26..302  
FT /label= N-glycosylation  
FT /label= Transmembrane\_domain  
FT Modified-site 39..44  
FT /label= N-myristoylation  
FT Modified-site 121..123  
FT /label= GPCR signal transduction site  
FT Modified-site 126..128  
FT /label= protein\_kinase\_C\_phosphorylation  
FT Modified-site 163..165  
FT /label= protein\_kinase\_C\_phosphorylation  
FT Modified-site 173..176  
FT /label= protein\_kinase\_phosphorylation  
FT Domain 303..342  
FT /label= Intracellular\_domain  
FT Modified-site 304..306  
FT /label= protein\_kinase\_C\_phosphorylation  
FT Modified-site 333..338  
FT /label= N-myristoylation  
XX  
XX WO200028028-A1.  
XX  
XX 18-MAY-2000.  
XX  
XX 05-NOV-1999; 99WO-US25956.  
XX  
XX 06-NOV-1998; 98US-0187134.  
XX 25-AUG-1999; 99US-0382918.  
XX  
XX (MILL-) MILLENNIUM PHARM INC.  
XX  
XX Glucksmann MA, Gu W, Welch NS;  
XX  
XX WPI; 2000-376543/32.  
XX N-PSDB; AA27126.  
XX  
XX Identifying an agent modulating the level or activity of G-protein coupled receptor useful for screening a cell derived from a subject having disorders such as anaemia, neutropenia and thrombocytopenia -  
XX  
XX Disclosure; Page 88-89; 97pp; English.  
XX  
XX The present sequence shows the 15625 receptor protein. It is a novel G-coupled protein receptor (GPCR). The cDNA for this protein was isolated by screening a human cDNA library with sequences homologous to other GPCRs. The 15625 receptor protein is expressed in the glial cells of the brain. It is also expressed in several other tissues.  
XX The 15625 receptor protein may be useful for producing antibodies.  
XX which can be used to detect the presence of the receptor protein.  
XX The 15625 receptor protein polynucleotides are useful for generating probes, primers and antisense constructs. The polynucleotides encoding the 15625 receptor proteins can also be inserted into vectors to be used in gene therapy. The disorder that may be treated using the 15625 receptor protein polynucleotides and polypeptides include anaemia, neutropenia and thrombocytopenia.  
XX  
XX Sequence 342 AA;  
SQ

Query Match 100.0%; Score 1778; DB 21; Length 342;  
Best Local Similarity 100.0%; Pred. No. 5.3e-187;  
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQAVNLSAPGNTSLCTRDYKITQVLPFLYTVLFFVGLITNGLAMRFPQIRSKNFI 60  
DB 1 MQAVNLSAPGNTSLCTRDYKITQVLPFLYTVLFFVGLITNGLAMRFPQIRSKNFI 60  
QY 61 IFKNTVISDLMLITFFPKILSDAKLGTGRLTFVQVTSVIFFTNYISIFGLITI 120  
DB 61 IFKNTVISDLMLITFFPKILSDAKLGTGRLTFVQVTSVIFFTNYISIFGLITI 120

QY 121 DRYOKTRRPFKTSNPKNLGAKILSVVWAPMFLSLPNMILTNRPDRDNVKKCSFLKS 180  
DB 121 DRYOKTRRPFKTSNPKNLGAKILSVVWAPMFLSLPNMILTNRPDRDNVKKCSFLKS 180  
QY 181 EFGLVWHEIYNYICQVIFWIFNFIIVCYTLITKELYRSYVTRGVGKVPKKNVKVFI 240  
DB 181 EFGLVWHEIYNYICQVIFWIFNFIIVCYTLITKELYRSYVTRGVGKVPKKNVKVFI 240  
QY 241 IIAVFFICFVFPFHARIPYTLISQTRDVFDCVTAENTLFYVKESTLWLTSLNACLDPPFIYFF 300  
DB 241 IIAVFFICFVFPFHARIPYTLISQTRDVFDCVTAENTLFYVKESTLWLTSLNACLDPPFIYFF 300  
QY 301 LCKSFRNSLSMLKCPNSATSLSQDNRKKEQDGDGDPNEETPM 342  
DB 301 LCKSFRNSLSMLKCPNSATSLSQDNRKKEQDGDGDPNEETPM 342  
RESULT 5  
AAM79249  
ID AAM79249 standard; Protein; 342 AA.  
XX  
AC AAM79249;  
XX  
DT 06-NOV-2001 (first entry)  
XX  
DE Human protein SEQ ID NO 1911.  
XX  
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;  
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;  
KW tissue growth factor; immunomodulatory; cancer; leukaemia;  
KW nervous system disorder; arthritis; inflammation.  
XX  
OS Homo sapiens.  
XX  
PN WO200157190-A2.  
XX  
PD 09-AUG-2001.  
XX  
PF 05-FEB-2001; 2001WO-US04098.  
XX  
PR 03-FEB-2000; 2000US-0496914.  
PR 27-APR-2000; 2000US-0560875.  
PR 20-JUN-2000; 2000US-0598075.  
PR 19-JUL-2000; 2000US-0620325.  
PR 01-SEP-2000; 2000US-0654936.  
PR 15-SEP-2000; 2000US-0663561.  
PR 20-OCT-2000; 2000US-0693325.  
PR 30-NOV-2000; 2000US-0728422.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;  
PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;  
PI Xue AJ, Yang Y, Wehrman T, Goodrich R;  
XX  
DR WPI; 2001-476283/51.  
DR N-PSDB; AAK52382.  
XX  
PT Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy -  
XX  
PS Claim 20; Page 4310; 6221pp; English.  
XX  
CC The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAW80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and

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CC inflammation.
CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC (AAK80020) are omitted as the relevant pages from the sequence listing
CC were missing at the time of publication.
XX
XX
SQ Sequence 342 AA;

Query Match 100.0%; Score 1778; DB 22; Length 342;
Best Local Similarity 100.0%; Pred. No. 5.3e-187;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQAVNLTSAAGNTSLCTRDYKIQVLPFLYTVLFFVGLITNGLAMRIFQIRKSNFI 60
Db 1 MQAVNLTSAAGNTSLCTRDYKIQVLPFLYTVLFFVGLITNGLAMRIFQIRKSNFI 60
QY 61 IFLKNTVISDLMLITFFPKILSDAKLGTGLRTFVCOVTSVIFFTWYISIFLGLITI 120
Db 61 IFLKNTVISDLMLITFFPKILSDAKLGTGLRTFVCOVTSVIFFTWYISIFLGLITI 120
QY 121 DRYQKTRTPFKTSNPKNLLGAKILSVIWAFFMLTSLPMLITNRQPRDKNVKCSFLKS 180
Db 121 DRYQKTRTPFKTSNPKNLLGAKILSVIWAFFMLTSLPMLITNRQPRDKNVKCSFLKS 180
QY 181 EFLGVWHEIVNYICQVIFWFLNVLIVICVYITLITKELYSYVTRGVGVKVPKKNVNVKVI 240
Db 181 EFLGVWHEIVNYICQVIFWFLNVLIVICVYITLITKELYSYVTRGVGVKVPKKNVNVKVI 240
QY 241 IIAVFFICFVPHFARIPYTLISQTRDVPDCTAENTLFYVKESTLWLSLNACLDPPFIYFF 300
Db 241 IIAVFFICFVPHFARIPYTLISQTRDVPDCTAENTLFYVKESTLWLSLNACLDPPFIYFF 300
QY 301 LCKSFNLSLSMLKCPNSATLSQDNKKKQGGDPNEETPM 342
Db 301 LCKSFNLSLSMLKCPNSATLSQDNKKKQGGDPNEETPM 342

RESULT 6
AAE04386
ID AAE04386 standard; Protein; 342 AA.
AC AAE04386;
XX
XX 04-SEP-2001 (first entry)
XX
XX Human P2-purinergic receptor subtype, P2Y12.
XX
XX Human; P2-purinergic receptor; P2Y12; cardiant; vasotropic; thrombolytic;
XX cerebroprotective; synaecological; ADP; adenosine 5'-diphosphate; angina;
XX myocardial infarction; ischaemic attack; preecclampsia; bleeding disorder;
XX carotid endarterectomy; vascular graft surgery; brain disorder; migraine;
XX vascular injury; schizophrenia; eating disorder; depression; angioplasty;
XX peripheral vascular disease; platelet aggregation; restenotic; embolism;
XX thrombocytopenic purpura; stroke; pertussis toxin-sensitive G protein;
XX Gi; disseminated intravascular coagulation; thrombosis.
XX
OS Homo sapiens.
XX
XX Key
XX Location/Qualifiers
XX Domain
XX 27..50
XX /label= Transmembrane_domain_1
XX 58..82
XX /label= Transmembrane_domain_2
XX 97..121
XX /label= Transmembrane_domain_3
XX 140..163
XX /label= Transmembrane_domain_4
XX 189..213
XX /label= Transmembrane_domain_5
XX 234..259
XX /label= Transmembrane_domain_6
XX 278..303
XX /label= Transmembrane_domain_7
XX

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PN WC0200146454-A1.
XX
XX 28-JUN-2001.
XX
XX 26-DEC-2000; 2000WO-US34998.
XX
XX 23-DEC-1999; 99US-0171622.
XX
XX (CORT-) COR THERAPEUTICS INC.
XX
XX Conley PB, Jantzen H, Ramakrishnan-Dubridge V, Julius DJ;
XX Hollloper G;
XX
XX WPI; 2001-418082/44.
XX N-PSDB; AAD08695.
XX
XX Novel isolated ADP receptor, termed P2Y12 receptor polypeptide, useful
XX for identifying binding partners and for diagnostic applications -
XX
XX Example 1; Fig 5A; 108pp; English.
XX
XX The invention relates to ADP (adenosine 5'-diphosphate) receptor, termed
XX as P2Y12 receptor and its corresponding cDNA molecule. P2Y12 receptor is
XX the subtype of P2-purinergic receptor. The P2Y12 receptor is expressed
XX selectively in the platelets and brain, and couples to a pertussis toxin-
XX sensitive G protein (Gi). P2Y12 receptor is a G protein-coupled receptor
XX that responds to ADP. The invention also relates to a method for
XX identifying an agent which is useful for modulating acute myocardial
XX infarction, unstable angina, chronic stable angina, transient ischaemic
XX attacks, strokes, peripheral vascular disease, preecclampsia, deep venous
XX thrombosis, embolism, disseminated intravascular coagulation, thrombotic
XX thrombocytopenic purpura or a bleeding disorder; thrombotic and
XX restenotic complications following angioplasty, carotid endarterectomy,
XX post CABG (coronary artery bypass graft) surgery, vascular graft surgery,
XX stent placements or insertion of endovascular devices and prostheses.
XX P2Y12 receptor is useful for identifying binding partners and for
XX diagnostic applications. P2Y12 receptor provides targets for screening
XX synthetic small molecules and combinatorial or naturally occurring
XX compound libraries to regulate platelet aggregation, vascular injury, or
XX disease as well as schizophrenia, eating disorders, depression, migraine
XX and other brain disorders. The present sequence is human P2-purinergic
XX receptor subtype, referred as P2Y12.
XX
XX Sequence 342 AA;

Query Match 100.0%; Score 1778; DB 22; Length 342;
Best Local Similarity 100.0%; Pred. No. 5.3e-187;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQAVNLTSAAGNTSLCTRDYKIQVLPFLYTVLFFVGLITNGLAMRIFQIRKSNFI 60
Db 1 MQAVNLTSAAGNTSLCTRDYKIQVLPFLYTVLFFVGLITNGLAMRIFQIRKSNFI 60
QY 61 IFLKNTVISDLMLITFFPKILSDAKLGTGLRTFVCOVTSVIFFTWYISIFLGLITI 120
Db 61 IFLKNTVISDLMLITFFPKILSDAKLGTGLRTFVCOVTSVIFFTWYISIFLGLITI 120
QY 121 DRYQKTRTPFKTSNPKNLLGAKILSVIWAFFMLTSLPMLITNRQPRDKNVKCSFLKS 180
Db 121 DRYQKTRTPFKTSNPKNLLGAKILSVIWAFFMLTSLPMLITNRQPRDKNVKCSFLKS 180
QY 181 EFLGVWHEIVNYICQVIFWFLNVLIVICVYITLITKELYSYVTRGVGVKVPKKNVNVKVI 240
Db 181 EFLGVWHEIVNYICQVIFWFLNVLIVICVYITLITKELYSYVTRGVGVKVPKKNVNVKVI 240
QY 241 IIAVFFICFVPHFARIPYTLISQTRDVPDCTAENTLFYVKESTLWLSLNACLDPPFIYFF 300
Db 241 IIAVFFICFVPHFARIPYTLISQTRDVPDCTAENTLFYVKESTLWLSLNACLDPPFIYFF 300
QY 301 LCKSFNLSLSMLKCPNSATLSQDNKKKQGGDPNEETPM 342
Db 301 LCKSFNLSLSMLKCPNSATLSQDNKKKQGGDPNEETPM 342

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	Query Match	100.0%	Score 1778;	DB 23;	Length 342;
	Best Local Similarity	100.0%;	Pred No 5 3e-187;		
	Matches 342;	Conservative	0;	Mismatches	0;
				Indels	Gaps
Qy	1	MQAVNLSAPGNTSLCTRDYKTIQVIFLLYVFLFVGLITNGLAMRLEFQIRKSNFI	60		
Db	1	MQAVNLSAPGNTSLCTRDYKTIQVIFLLYVFLFVGLITNGLAMRLEFQIRKSNFI	60		
Qy	61	IFLNTVSDLLMLTPPPKILSDAKIGTGPLTFVCQVTSVIFYTMKISISIFGLITI	120		
Db	61	IFLNTVSDLLMLTPPPKILSDAKIGTGPLTFVCQVTSVIFYTMKISISIFGLITI	120		
Qy	121	DYQKTRPFTKSNPKNLGAKILSVVIWAPMFLSLFNMLTNRPDRDNVKKCSFLKS	180		
Db	121	DYQKTRPFTKSNPKNLGAKILSVVIWAPMFLSLFNMLTNRPDRDNVKKCSFLKS	180		
Qy	181	EFLGVNHEIIVNYICQVIFWINFLIVICYTLITIKELYSVTRGVKVPKKNVKVFI	240		
Db	181	EFLGVNHEIIVNYICQVIFWINFLIVICYTLITIKELYSVTRGVKVPKKNVKVFI	240		

	Query Match	100.0%;	Score 1778;	DB 23;	Length 342;
	Best Local Similarity	100.0%;	Pred. No. 5.3e-187;		
	Matches 342;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MQAVNLTSAPGNTSLCTRDYKIKQVLPFLYTVLFFVGLITNGLAMRFFQIRSKSNFI	60		
Db	1	MQAVNLTSAPGNTSLCTRDYKIKQVLPFLYTVLFFVGLITNGLAMRFFQIRSKSNFI	60		
QY	61	IFLKNVTISDLLMITFPFKILSDAKLGTGRLTFVQVTSVIFYTMYTISIFLGLTII	120		
Db	61	IFLKNVTISDLLMITFPFKILSDAKLGTGRLTFVQVTSVIFYTMYTISIFLGLTII	120		
QY	121	DYQKTRTPFKTSNPKNLLGAKILSVVIWAPMFLSLPNMILNTRPRDNKVKKCSFLKS	180		
Db	121	DYQKTRTPFKTSNPKNLLGAKILSVVIWAPMFLSLPNMILNTRPRDNKVKKCSFLKS	180		
QY	181	EFLVWHELVNVIQVIEWIFLVIVVCYTLITKELYRSVVRTRGVGVKPRKKNVKYFI	240		
Db	181	EFLVWHELVNVIQVIEWIFLVIVVCYTLITKELYRSVVRTRGVGVKPRKKNVKYFI	240		



QY 241 IIAVFFICFVFPFHARIPYTLQTRDVFDCDAENTLFYVKESTLWLTSLNACLDPIYFF 300  
DB 241 IIAVFFICFVFPFHARIPYTLQTRDVFDCDAENTLFYVKESTLWLTSLNACLDPIYFF 300  
QY 301 LCKSPRSLISMLKCPNSATSLSDNRKKKQDGGDPNEETPM 342  
DB 301 LCKSPRSLISMLKCPNSATSLSDNRKKKQDGGDPNEETPM 342

RESULT 9  
AAU80164  
ID AAU80164 standard; Protein; 342 AA.  
XX AAU80164;  
XX  
DT 15-JUL-2002 (first entry)  
XX  
DE Human ADP-glucose receptor.  
XX  
KW Human; ADP-glucose; receptor; G protein-coupled receptor;  
KW agonist; antagonist; cardiovascular function disorder; vasorelaxation;  
KW ischaemia; angina pectoris; gastrointestinal disorder; diarrhoea;  
KW immune disorder; immunodeficiency disorder; autoimmune disorder;  
KW rheumatoid arthritis; bacterial infection; viral infection;  
KW fungal infection; protozoal infection; respiratory disorder; asthma;  
KW kidney disorder; glomerulonephritis; hepatobiliary disorder; cirrhosis;  
KW endocrine disorder; adrenal dysfunction; musculoskeletal disorder;  
KW osteoporosis; nervous system disorder; Alzheimer's disease;  
KW psychotic disorder; depression; cancer; pain; glycogen storage disease;  
KW disorder of body weight; AIDS; acquired immunodeficiency syndrome;  
KW chromosome 3; Usher's syndrome type 3.  
XX  
CS Homo sapiens.  
XX  
FN WO200224942-A2.  
XX  
PD 28-MAR-2002.  
XX  
PF 19-SEP-2001; 2001WO-US29523.  
XX  
PR 20-SEP-2000; 2000US-234025P.  
PR 09-FEB-2001; 2001US-0780576.  
XX  
XX (REGC ) UNIV CALIFORNIA.  
XX  
XX Civelli O, Nothacker H, Wang Z, Reinscheid R;  
XX  
DR WPI; 2002-383195/41.  
DR N-PSDB; ABK50286.  
XX  
PT Identifying an agonist, antagonist or ligand of an ADP-glucose  
PT receptor, for treating cardiovascular, gastrointestinal, kidney,  
PT endocrine, immune disorders, and bacterial, viral, protozoal or fungal  
PT infections  
XX  
PS Claim 3; Fig 1; 86pp; English.

The invention relates to identifying an ADP-glucose (ADP-G) receptor (a G protein-coupled receptor) agonist, antagonist or ligand, comprises contacting the receptor with one or more candidate compounds so that the receptor produces a G protein-coupled signal in response to ADP-G or selectively binds ADP-G, and identifying the candidate molecule that alters signal production as an agonist, antagonist or binds as a ligand. Also included are altering signalling through an ADP-G receptor, by contacting a cell expressing the receptor with ADP-G or the ant/agonist, ameliorating an ADP-G receptor associated condition, by administering a therapeutic composition comprising ADP-G or the ant/agonist to an individual and a composition comprising the ADP\_G receptor and ADP-G. ADP-G or the ant/agonist is useful for treating an ADP-G receptor associated condition e.g. cardiovascular function disorder, where the therapeutic composition induces vasorelaxation. The new methods are useful in identifying ant/agonists and ligands of the receptor.

The ant/agonists are useful therapeutically for preventing or ameliorating conditions associated with the receptor such as cardiovascular disorders (e.g. ischaemia, hypertension, hypotension, angina pectoris, myocardial infarction, stroke, congestive heart failure, shock, erectile dysfunction, orthostatic intolerance and migraine), gastrointestinal disorders (e.g. diarrhoea, gastritis, inflammatory bowel disease), immune disorders (e.g. immunodeficiency disorders, autoimmune disorders, rheumatoid arthritis), infections caused by bacteria, fungi, protozoa or virus, respiratory disorders (e.g. asthma, pneumonia, bronchitis), kidney disorders (e.g. glomerulonephritis, renal failure, lupus), hepatobiliary disorders (e.g. jaundice, cirrhosis, hepatitis), endocrine disorders (e.g. pituitary, thyroid or adrenal dysfunctions), musculoskeletal disorders (e.g. osteoporosis, muscular dystrophies), nervous system disorders (e.g. Parkinson's and Alzheimer's disease), pain, glycogen storage depression, anxiety, schizophrenia), pain, glycogen storage diseases and disorders of body weight (e.g. as a result of cancer or AIDS, acquired immunodeficiency syndrome). The gene for the ADP-G receptor is located on chromosome 3 in a region associated with Usher syndrome type 3 (progressive hearing loss). The ligand is useful therapeutically, in detecting normal or abnormal expression of the receptor in an isolated sample or in vivo diagnostic imaging procedures, and targeting specifically a diagnostic group to cells and tissues that express the receptor. The present sequence represents the ADP-G receptor.

XX  
SQ Sequence 342 AA;  
Query Match 100.0%; Score 1778; DB 23; Length 342;  
Best Local Similarity 100.0%; Pred. No. 5.3e-187;  
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOAVDNLTSAPONTSLCTRDYKIQVLPFLLYTLVFFVGLITNGLAMRIFPQIRSKNFI 60  
DB 1 MOAVDNLTSAPONTSLCTRDYKIQVLPFLLYTLVFFVGLITNGLAMRIFPQIRSKNFI 60  
QY 61 IFLKNTVISDLLMLTTPFPKILSDAKLGTGPRFVCOVTSVIFPYTMYISIFLGLITI 120  
DB 61 IFLKNTVISDLLMLTTPFPKILSDAKLGTGPRFVCOVTSVIFPYTMYISIFLGLITI 120  
QY 121 DRYQKTRTPFKTSNPKNLLGAKILSVIWAFWLISLPNMLITNRQPKDNKVKCSFLKS 180  
DB 121 DRYQKTRTPFKTSNPKNLLGAKILSVIWAFWLISLPNMLITNRQPKDNKVKCSFLKS 180  
QY 181 EFLVWHEIVNYICQVIFWIFNLIVVCTYTLTKELYSYVTRTGKVPKKNVKVFI 240  
DB 181 EFLVWHEIVNYICQVIFWIFNLIVVCTYTLTKELYSYVTRTGKVPKKNVKVFI 240  
QY 241 IIAVFFICFVFPFHARIPYTLQTRDVFDCDAENTLFYVKESTLWLTSLNACLDPIYFF 300  
DB 241 IIAVFFICFVFPFHARIPYTLQTRDVFDCDAENTLFYVKESTLWLTSLNACLDPIYFF 300  
QY 301 LCKSPRSLISMLKCPNSATSLSDNRKKKQDGGDPNEETPM 342  
DB 301 LCKSPRSLISMLKCPNSATSLSDNRKKKQDGGDPNEETPM 342

RESULT 10  
AAU48353  
ID AAU48353 standard; Protein; 342 AA.  
XX  
XX AAU48353;  
XX  
DT 25-APR-2002 (first entry)  
XX  
DE Human G protein-coupled receptor, IGPCRI7.  
XX  
KW Human; G protein-coupled receptor; IGPCRI7; analgesic; neuroleptic;  
KW tranquiliser; antiparkinsonian; neuroprotective; nootropic;  
KW anticonvulsant; metabolic; anorectic; anabolic; antiinflammatory;  
KW antidiarheic; osteopathic; antistomatitic; antiallergic; antiarthritic;  
KW immunosuppressive; gene therapy; psychiatric disorder; schizophrenia;  
KW central nervous system disorder; movement dysfunction; schizophrenia;

KW multiple sclerosis; Alzheimer's disease; kidney disease; obesity;  
 KW gastrointestinal disorder; osteoporosis; infection;  
 KW gynecological disorder; receptor.  
 XX Homo sapiens.  
 OS  
 PN WO200202599-A2.  
 XX  
 PD 10-JAN-2002.  
 XX  
 PF 02-JUL-2001; 2001WO-EP07532.  
 XX  
 PR 30-JUN-2000; 2000US-215759P.  
 XX  
 PA (INGE-) INGENIUM PHARM AG.  
 XX  
 PI Wattler F, Wattler S, Trommler P, Nehls MC;  
 XX  
 DR WPI: 2002-140080/18.  
 DR N-PSDB; ABA98935.  
 XX  
 PT New human or mouse G protein-coupled receptor protein, IGPCR17, useful  
 PT for diagnosis, prevention, amelioration or treatment of central nervous  
 PT system disorders such as Tourette's syndrome, Parkinson's disease and  
 PT pain.  
 XX  
 PS Claim 8; Fig 2; 71pp; English.  
 XX  
 CC The present sequence is the protein sequence for human G protein-coupled  
 CC receptor (GPCR) protein, IGPCR17. The coding sequence for IGPCR17 is  
 CC useful in gene therapy for prevention, amelioration or treatment of  
 CC diseases characterised by aberrant expression or activity of IGPCR17,  
 CC where the disease is a psychiatric or central nervous system (CNS)  
 CC disorder associated with signal processing in CNS such as learning and  
 CC memory disorders, movement dysfunctions, tics, tremor, Tourette's  
 CC syndrome, Parkinson's disease, Huntington's disease, dyskinesias,  
 CC dystonia, pain and spasms. In addition, IGPCR17 and its coding sequence  
 CC are useful in diagnosis, prevention, amelioration or treatment of  
 CC diseases associated with signal processing in CNS, schizophrenia,  
 CC episodic paroxysmal anxiety (EPA) disorders such as obsessive compulsive  
 CC disorder (OCD), multiple sclerosis, Alzheimer's disease/dementia,  
 CC anorexia, kidney diseases such as renal failure, obesity,  
 CC gastrointestinal disorders such as irritable bowel syndrome (IBS),  
 CC diarrhoea, motility disorders and conditions of delayed gastric emptying,  
 CC osteoporosis, infections such as bacterial, fungal, protozoal and viral  
 CC infections, asthma, allergy, arthritis, sepsis and gynecological  
 CC disorders.  
 XX  
 SQ Sequence 342 AA;  
 Query Match 100.0%; Score 1778; DB 23; Length 342;  
 Best Local Similarity 100.0%; Pred. No. 5,3e-187;  
 Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MQAVDLNLTAPGNTSLCTRDYKITQVLPFLTYVLFVGLITNGLAMRIFQIRSKNFI 60  
 DB 1 MQAVDLNLTAPGNTSLCTRDYKITQVLPFLTYVLFVGLITNGLAMRIFQIRSKNFI 60  
 QY 61 IFLKNTVISDLMILTFPFKILSDAKLGTGPLRTFVQVTSVIFFTWYISIFGLITI 120  
 DB 61 IFLKNTVISDLMILTFPFKILSDAKLGTGPLRTFVQVTSVIFFTWYISIFGLITI 120  
 QY 121 DRYQKTRFPTKSNPKNLGAKILSVIWAFFLLSLPNMILTNQPRDKNVKCSFLKS 180  
 DB 121 DRYQKTRFPTKSNPKNLGAKILSVIWAFFLLSLPNMILTNQPRDKNVKCSFLKS 180  
 QY 181 EFLGVWHEIVNYICQVIFINFLIVICVTLTKELYSYVTRGVGKPRKKNVKYFI 240  
 DB 181 EFLGVWHEIVNYICQVIFINFLIVICVTLTKELYSYVTRGVGKPRKKNVKYFI 240  
 QY 241 IIAVFFICVDFHFAPIPTLSOTRVDFCTAENTLFYVKESTLMTLSNACLDPIYFF 300  
 DB 241 IIAVFFICVDFHFAPIPTLSOTRVDFCTAENTLFYVKESTLMTLSNACLDPIYFF 300

QY 301 LCKSPRNSLIMLKCPNSATSLSDNRKKEQGGDPNEETPM 342  
 DB 301 LCKSPRNSLIMLKCPNSATSLSDNRKKEQGGDPNEETPM 342  
 RESULT 11  
 ID ABB05031 standard; Protein; 342 AA.  
 XX  
 AC ABB05031;  
 XX  
 DT 25-MAR-2002 (first entry)  
 XX  
 DE Human SP168 receptor protein SEQ ID NO:2.  
 XX  
 KW Human; SP168 receptor; mammalian G-Protein coupled receptor; GPCR;  
 KW neurodegenerative disorder; Parkinson's disease; Alzheimer's disease;  
 KW Huntington's disease; amyotrophic lateral sclerosis; ALS; MS; receptor;  
 KW multiple sclerosis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2001046497-A1.  
 XX  
 PD 29-NOV-2001.  
 XX  
 PF 16-APR-2001; 2001US-0835922.  
 XX  
 PR 21-APR-2000; 2000US-199041P.  
 XX  
 PA (ZHAN/) ZHANG F L.  
 PA (LUOL/) LUO L.  
 PA (GUST/) GUSTAFSON E.  
 PA (LIUY/) LIU Y.  
 PA (CHEN/) CHEN G.  
 XX  
 PI Zhang FL, Luo L, Gustafson E, Liu Y, Chen G;  
 XX  
 DR WPI: 2002-082414/11.  
 DR N-PSDB; ABA92641.  
 XX  
 PT Identifying modulators of mammalian G-Protein Coupled Receptor SP168,  
 PT useful for treating Parkinson's Disease, Alzheimer's Disease,  
 PT Huntington's Disease, amyotrophic lateral sclerosis and multiple  
 PT sclerosis -  
 XX  
 PS Claim 3; Page 14-15; 16pp; English.  
 XX  
 CC The present invention describes a method for identifying agonists and  
 CC antagonists of mammalian G-Protein Coupled Receptor (GPCR) SP168 which  
 CC may be used to treat neurodegenerative disorders. The method comprises:  
 CC (a) contacting a mammalian SP168 receptor (or a functional fragment) in  
 CC the presence of a known amount of a labeled SP168 receptor ligand with  
 CC a sample to be tested for the presence of the SP168 receptor agonist or  
 CC antagonist; and (b) measuring the amount of labeled SP168 ligand  
 CC specifically bound to the receptor (the SP168 receptor agonist or  
 CC antagonist in the sample is identified by measuring the difference in  
 CC binding of the labeled SP168 receptor ligand to the receptor, compared  
 CC to what would be measured in the absence of such agonist or antagonist).  
 CC The method is used to detect agonists and antagonists (especially  
 CC antibodies) of the SP168 GPCR which may be used to treat a  
 CC neurodegenerative disorder, such as Parkinson's Disease, Alzheimer's  
 CC Disease, Huntington's Disease, amyotrophic lateral sclerosis (ALS) and  
 CC multiple sclerosis (MS) in mammals, especially humans. The present  
 CC sequence represents the human SP168 receptor which can be used in the  
 CC method of the invention.  
 XX  
 SQ Sequence 342 AA;

Query Match 100.0%; Score 1778; DB 23; Length 342;  
 Best Local Similarity 100.0%; Pred. No. 5,3e-187;  
 Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQAVDNLTSAPGNTSLCTRDYKIKITQVLPFLLYTVLFFVGLITNGLAMRIFPQIRSKSNFI 60  
 Db 1 MQAVDNLTSAPGNTSLCTRDYKIKITQVLPFLLYTVLFFVGLITNGLAMRIFPQIRSKSNFI 60  
 QY 61 IFLKNTVISDLLMLTTPFKILSDAKLGTGRLTFCVQVTSVIFFTMYISISFLGLITI 120  
 Db 61 IFLKNTVISDLLMLTTPFKILSDAKLGTGRLTFCVQVTSVIFFTMYISISFLGLITI 120  
 QY 121 DRYQKTRTPFKTSNPKNLLGAKILSVVWAFMFLSLPNMILNRPDRQNVKCKSFLKS 180  
 Db 121 DRYQKTRTPFKTSNPKNLLGAKILSVVWAFMFLSLPNMILNRPDRQNVKCKSFLKS 180  
 QY 181 EFGLVWHEIYVNYICQVIFWFLNFIIVCYTLITKELYSVVRTRGVKVPKKNVKKVFI 240  
 Db 181 EFGLVWHEIYVNYICQVIFWFLNFIIVCYTLITKELYSVVRTRGVKVPKKNVKKVFI 240  
 QY 241 IIAVFFICFVFPFHARIPYTLISQTRDVFDCVTAENTLFYVKESTLWLTSLNACLDPIYFF 300  
 Db 241 IIAVFFICFVFPFHARIPYTLISQTRDVFDCVTAENTLFYVKESTLWLTSLNACLDPIYFF 300  
 QY 301 LCKSFRNSLISMLKCPNSATSLSDNRKKEQDGDNPNEETPM 342  
 Db 301 LCKSFRNSLISMLKCPNSATSLSDNRKKEQDGDNPNEETPM 342  
 RESULT 12  
 AAG80236  
 ID AAG80236 standard; Protein; 342 AA.  
 AC AAG80236;  
 XX  
 DT 24-JAN-2002 (first entry)  
 XX  
 DE Human PAFR3 protein.  
 XX  
 KW PAFR-3; platelet activating factor receptor; human; chromosome 3;  
 KW thrombocyte activation; hypotension; renal permeability;  
 KW bronchoconstriction; transgenic animal; knockout animal.  
 XX  
 OS Homo sapiens.  
 XX  
 PN DE10020073-A1.  
 XX  
 PD 25-OCT-2001.  
 XX  
 PF 22-APR-2000; 2000DE-1020073.  
 XX  
 PR 22-APR-2000; 2000DE-1020073.  
 XX  
 PA (BRUE/) BRUESS M.  
 PA (BOEN/) BOENISCH H.  
 FI Bruess M, Boenisch H;  
 XX  
 DR WPI; 2002-027296/04.  
 DR N-PSDB; AAI68802, AAI68803.  
 XX  
 PT New human platelet-activating factor (PAF) receptor-3 gene, useful for  
 diagnosis and treatment of PAF-related diseases  
 XX  
 PS Disclosure; Page 4; 6pp; German.  
 XX  
 CC This invention describes a novel human platelet-activating factor (PAF)  
 CC receptor-3 (PAFR-3) gene (I). The protein encoded by (I) probably  
 CC modulates the activity of PAF, which is involved in many  
 CC (patho)physiological processes, e.g., thrombocyte activation,  
 CC hypotension, increased vascular permeability, bronchoconstriction etc.  
 CC (I), and derived (anti)sense oligonucleotides, are useful in the  
 CC treatment and diagnosis of (I)-related diseases; for producing  
 CC transgenic/knockout animals, and for recombinant expression of the  
 CC protein (II) that it encodes. (II) is useful in ligand-binding studies  
 CC and screening assays, also for treatment and diagnosis of (II)-related

CC diseases. This sequence represents the human platelet-activating  
 CC factor receptor (PAFR-3) protein described in the invention.  
 XX  
 SQ Sequence 342 AA;  
 Query Match 100.0%; Score 1778; DB 23; Length 342;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-187;  
 Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MQAVDNLTSAPGNTSLCTRDYKIKITQVLPFLLYTVLFFVGLITNGLAMRIFPQIRSKSNFI 60  
 Db 1 MQAVDNLTSAPGNTSLCTRDYKIKITQVLPFLLYTVLFFVGLITNGLAMRIFPQIRSKSNFI 60  
 QY 61 IFLKNTVISDLLMLTTPFKILSDAKLGTGRLTFCVQVTSVIFFTMYISISFLGLITI 120  
 Db 61 IFLKNTVISDLLMLTTPFKILSDAKLGTGRLTFCVQVTSVIFFTMYISISFLGLITI 120  
 QY 121 DRYQKTRTPFKTSNPKNLLGAKILSVVWAFMFLSLPNMILNRPDRQNVKCKSFLKS 180  
 Db 121 DRYQKTRTPFKTSNPKNLLGAKILSVVWAFMFLSLPNMILNRPDRQNVKCKSFLKS 180  
 QY 181 EFGLVWHEIYVNYICQVIFWFLNFIIVCYTLITKELYSVVRTRGVKVPKKNVKKVFI 240  
 Db 181 EFGLVWHEIYVNYICQVIFWFLNFIIVCYTLITKELYSVVRTRGVKVPKKNVKKVFI 240  
 QY 241 IIAVFFICFVFPFHARIPYTLISQTRDVFDCVTAENTLFYVKESTLWLTSLNACLDPIYFF 300  
 Db 241 IIAVFFICFVFPFHARIPYTLISQTRDVFDCVTAENTLFYVKESTLWLTSLNACLDPIYFF 300  
 QY 301 LCKSFRNSLISMLKCPNSATSLSDNRKKEQDGDNPNEETPM 342  
 Db 301 LCKSFRNSLISMLKCPNSATSLSDNRKKEQDGDNPNEETPM 342  
 RESULT 13  
 ABP81734  
 ID ABP81734 standard; Protein; 342 AA.  
 XX  
 AC ABP81734;  
 XX  
 DT 04-MAR-2003 (first entry)  
 XX  
 DE Human P2Y12 platelet ADP receptor protein SEQ ID NO:643.  
 XX  
 KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;  
 KW G protein-coupled receptor modulator; antibody; immune-related disease;  
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;  
 KW immunological-related cell proliferative disease; autoimmune disease;  
 KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;  
 KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;  
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;  
 KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;  
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;  
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;  
 KW ulcer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200261087-A2.  
 XX  
 PD 08-AUG-2002.  
 XX  
 PF 19-DEC-2001; 2001WO-US50107.  
 XX  
 PR 19-DEC-2000; 2000US-257144P.  
 XX  
 PA (LIFE-) LIFESPAN BIOSCIENCES INC.  
 XX  
 PI Burner GC, Roush CL, Brown JP;  
 XX  
 DR WPI; 2003-046718/04.  
 DR N-PSDB; ABZ42580.  
 XX

PT New isolated antigenic peptides e.g., for G protein-coupled receptors  
PT (GPCR), useful for diagnosing and designing drugs for treating  
PT conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease,  
PT cancer or autoimmune diseases  
XX Disclosure; Fig 1; 523pp; English.  
PS  
XX  
CC The present invention describes antigenic peptides (I) comprising:  
CC (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino  
CC acids. Also described: (1) an assay for the detection of a particular  
CC G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;  
CC and (2) an isolated antibody having high specificity and high affinity  
CC or avidity for a particular GPCR. (1) can be used as GPCR modulators and  
CC in gene therapy. The antigenic peptides for GPCRs are useful in detecting  
CC an antibody against a particular GPCR, and in the production of specific  
CC antibodies. The peptides and antibodies are also useful for detecting the  
CC presence or absence of corresponding GPCRs. The antigenic peptides for  
CC GPCRs and antibodies are useful for diagnosing and designing drugs for  
CC treating immune-related diseases, growth-related diseases, cell  
CC regeneration-related diseases, immunological-related cell proliferative  
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,  
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,  
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute  
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host  
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,  
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory  
CC loss, epilepsy, asthma, tuberculosis, obesity, diabetes, hypertension,  
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or  
CC any other disorder in which GPCRs are involved. The antibodies may be  
CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode  
CC GPCR proteins given in ABP1675 to ABP82018, which are used in the  
CC exemplification of the present invention.  
XX  
XX Sequence 342 AA;  
SQ  
Query Match 100.0%; Score 1778; DB 24; Length 342;  
Best Local Similarity 100.0%; Pred. No. 5.3e-187;  
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MQAVNLTSAAGNTSLCTRDYKKTQVLPFLYTVLFFVGLITNGLAMRIFFOIRSKSNFI 60  
Db 1 MQAVNLTSAAGNTSLCTRDYKKTQVLPFLYTVLFFVGLITNGLAMRIFFOIRSKSNFI 60  
QY 61 IFLKNTVISDLMLITFFPKILSDAKLGTGRLTFVCOVTSVIFFTMYISISFLGLITI 120  
Db 61 IFLKNTVISDLMLITFFPKILSDAKLGTGRLTFVCOVTSVIFFTMYISISFLGLITI 120  
QY 121 DRYQKTTTRPFKTSNPKNLGAKILSVIWAFFLLSLPNMILTNRQPRDKNNKCSFLKS 180  
Db 121 DRYQKTTTRPFKTSNPKNLGAKILSVIWAFFLLSLPNMILTNRQPRDKNNKCSFLKS 180  
QY 181 EFLGVWHEIVNYICQVIFWIFNLIVICVTLITKELYSYVTRGVGVPRKKNVKVFI 240  
Db 181 EFLGVWHEIVNYICQVIFWIFNLIVICVTLITKELYSYVTRGVGVPRKKNVKVFI 240  
QY 241 IIAVFFICFVPHFARIPTLTSQTRDVFDCVAENTLFVVKESTLWLTSLNACLDPFYIFF 300  
Db 241 IIAVFFICFVPHFARIPTLTSQTRDVFDCVAENTLFVVKESTLWLTSLNACLDPFYIFF 300  
QY 301 LCKSFNSLSMLKCPNSATSLSQNRKKEQGGDPNEETPM 342  
Db 301 LCKSFNSLSMLKCPNSATSLSQNRKKEQGGDPNEETPM 342  
RESULT 14.  
ID AAY94445  
XX AAY94445 standard; Protein; 342 AA.  
AC  
XX AAY94445;  
XX  
DT 21-AUG-2000 (first entry)  
DE Macaque ortholog of human 15625 receptor protein.

XX Human; G-protein-coupled receptor; GPCR; 15625 receptor protein;  
KW glial cells; spleen; colon; liver; brain; T-cell; heart;  
KW red cell; thymus; B-cell; pancreas; disorder; chromosome 3;  
KW anaemia; neutropenia; thrombocytopenia; gene therapy; ss.  
XX  
OS Macaca sp.  
XX  
XX WC200028028-A1.  
XX  
PD 18-MAY-2000.  
XX  
XX 05-NOV-1999; 99WO-US25956.  
XX  
XX 06-NOV-1998; 98US-0187134.  
PR 25-AUG-1999; 99JUS-0382918.  
XX  
XX (WILL-) MILLENNIUM PHARM INC.  
XX  
XX Glucksmann MA, Gu W, Welch NS;  
PI WPI; 2000-376543/32.  
DR N-PSDB; AAA27127.  
XX  
XX Identifying an agent modulating the level or activity of G-protein  
XX coupled receptor useful for screening a cell derived from a subject  
XX having disorders such as anaemia, neutropenia and thrombocytopenia  
XX  
XX Disclosure; Page 90-92; 97pp; English.  
XX  
XX The 15625 receptor protein is a novel G-coupled protein receptor (GPCR).  
XX The cDNA for this protein was isolated by screening a human cDNA library  
XX with sequences homologous to other GPCRs. The 15625 receptor protein is  
XX expressed in the glial cells of the brain. It is also expressed in  
XX several other tissues. The 15625 receptor protein may be useful for  
XX producing antibodies which can be used to detect the presence of the  
XX receptor protein. The 15625 receptor protein polynucleotides are useful  
XX for generating probes, primers and antisense constructs. The  
XX polynucleotides encoding the 15625 receptor proteins can also be inserted  
XX into vectors to be used in gene therapy. The disorder that may be  
XX treated using the 15625 receptor protein polynucleotides and  
XX polypeptides include anaemia, neutropenia and thrombocytopenia. The  
XX present sequence is the macaque ortholog of the human 15625 receptor  
XX protein.  
XX  
XX Sequence 342 AA;  
SQ  
Query Match 98.3%; Score 1748; DB 21; Length 342;  
Best Local Similarity 98.0%; Pred. No. 1.1e-183;  
Matches 335; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
QY 1 MQAVNLTSAAGNTSLCTRDYKKTQVLPFLYTVLFFVGLITNGLAMRIFFOIRSKSNFI 60  
Db 1 MQAVNLTSAAGNTSLCTRDYKKTQVLPFLYTVLFFVGLITNGLAMRIFFOIRSKSNFI 60  
QY 61 IFLKNTVISDLMLITFFPKILSDAKLGTGRLTFVCOVTSVIFFTMYISISFLGLITI 120  
Db 61 IFLKNTVISDLMLITFFPKILSDAKLGTGRLTFVCOVTSVIFFTMYISISFLGLITI 120  
QY 121 DRYQKTTTRPFKTSNPKNLGAKILSVIWAFFLLSLPNMILTNRQPRDKNNKCSFLKS 180  
Db 121 DRYQKTTTRPFKTSNPKNLGAKILSVIWAFFLLSLPNMILTNRQPRDKNNKCSFLKS 180  
QY 181 EFLGVWHEIVNYICQVIFWIFNLIVICVTLITKELYSYVTRGVGVPRKKNVKVFI 240  
Db 181 EFLGVWHEIVNYICQVIFWIFNLIVICVTLITKELYSYVTRGVGVPRKKNVKVFI 240  
QY 241 IIAVFFICFVPHFARIPTLTSQTRDVFDCVAENTLFVVKESTLWLTSLNACLDPFYIFF 300  
Db 241 IIAVFFICFVPHFARIPTLTSQTRDVFDCVAENTLFVVKESTLWLTSLNACLDPFYIFF 300  
QY 301 LCKSFNSLSMLKCPNSATSLSQNRKKEQGGDPNEETPM 342  
Db 301 LCKSFNSLSMLKCPNSATSLSQNRKKEQGGDPNEETPM 342

301 LCKSPRNSLISMLKCPNSATSQSDNRKKEQDGPNEETPM 342

RESULT 15

AAE04385

ID AAE04385 standard; Protein; 315 AA.

XX AAE04385;

AC AAE04385;

DT 04-SEP-2001 (first entry)

DE Human P2-purinegic receptor subtype, P2Y12 protein fragment.

XX Human; P2-purinegic receptor; P2Y12; cardiant; vasotropic; thrombolytic;  
 KW cerebroprotective; synaecological; ADP; adenosine 5'-diphosphate; angina;  
 KW myocardial infarction; ischaemic attack; preelampsia; bleeding disorder;  
 KW carotid endarterectomy; vascular graft surgery; brain disorder; migraine;  
 KW vascular injury; schizophrenia; eating disorder; depression; angioplasty;  
 KW peripheral vascular disease; platelet aggregation; restenotic; embolism;  
 KW thrombocytopenic purpura; stroke; pertussis toxin-sensitive G protein;  
 KW Gi; disseminated intravascular coagulation; thrombosis.

XX Homo sapiens.

OS WO200146454-A1.

XX 28-JUN-2001.

PF 26-DEC-2000; 2000WO-US34998.

XX 23-DEC-1999; 99US-0171622.

PR (CORT-) COR THERAPEUTICS INC.

XX Conley PB, Jantzen H, Ramakrishnan-Dubridge V, Julius DJ;

PI Hollopetter G;

XX WPI; 2001-418082/44.

DR N-PSDB; AAD08694.

XX Novel isolated ADP receptor, termed P2Y12 receptor polypeptide, useful  
 PT for identifying binding partners and for diagnostic applications -  
 XX Example 1; Page 84-85; 108pp; English.

PS The invention relates to ADP (adenosine 5'-diphosphate) receptor, termed  
 CC as P2Y12 receptor and its corresponding cDNA molecule. P2Y12 receptor is  
 CC the subtype of P2-purinegic receptor. The P2Y12 receptor is expressed  
 CC selectively in the platelets and brain, and couples to a pertussis toxin-  
 CC sensitive G protein (Gi). P2Y12 receptor is a G protein-coupled receptor  
 CC that responds to ADP. The invention also relates to a method for  
 CC identifying an agent which is useful for modulating acute myocardial  
 CC infarction, unstable angina, chronic stable angina, transient ischaemic  
 CC attacks, strokes, peripheral vascular disease, preelampsia, deep venous  
 CC thrombosis, embolism, disseminated intravascular coagulation, thrombotic  
 CC thrombocytopenic purpura or a bleeding disorder; thrombotic and  
 CC restenotic complications following angioplasty, carotid endarterectomy,  
 CC post CABG (coronary artery bypass graft) surgery, vascular graft surgery,  
 CC stent placements or insertion of endovascular devices and prostheses.  
 CC P2Y12 receptor is useful for identifying binding partners and for  
 CC diagnostic applications. P2Y12 receptor provides targets for screening  
 CC synthetic small molecules and combinatorial or naturally occurring  
 CC compound libraries to regulate platelet aggregation, vascular injury, or  
 CC disease as well as schizophrenia, eating disorders, depression, migraine  
 CC and other brain disorders. The present sequence is a fragment of human  
 CC P2-purinegic receptor subtype, referred as P2Y12.

XX Sequence 315 AA;

Query Match

Best Local Similarity 91.9%; Score 1634; DB 22; Length 315;

Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOAVDNLTSAFGNTSLCTRDYKIKITQVLPFLLYTVLFFVGLITNGLAMRIFFOIRSKSNFI 60  
 DB 1 MOAVDNLTSAFGNTSLCTRDYKIKITQVLPFLLYTVLFFVGLITNGLAMRIFFOIRSKSNFI 60  
 QY 61 IFKNTVISDLLMILTFFPKILSDAKLGTGPIRTFVCOVTSVIFVFTWYISISFLGLITI 120  
 DB 61 IFKNTVISDLLMILTFFPKILSDAKLGTGPIRTFVCOVTSVIFVFTWYISISFLGLITI 120  
 QY 121 DRYQKTRTPFKTSNPKNLLGAKILSVIWAFFMLLSLENMILTNRQPRDKNVKCSFLKS 180  
 DB 121 DRYQKTRTPFKTSNPKNLLGAKILSVIWAFFMLLSLENMILTNRQPRDKNVKCSFLKS 180  
 QY 181 EFGVWHELVNYICQVIFWNLIVIVCVTLITKELYSYVTRGVGKVPKKNVKVFI 240  
 DB 181 EFGVWHELVNYICQVIFWNLIVIVCVTLITKELYSYVTRGVGKVPKKNVKVFI 240  
 QY 241 IIAVFFICFVPPFPHFARIPTVLSQTRDVFDCVTAENTLFTVKESTLWLTSLNACLDPPFIYFF 300  
 DB 241 IIAVFFICFVPPFPHFARIPTVLSQTRDVFDCVTAENTLFTVKESTLWLTSLNACLDPPFIYFF 300  
 QY 301 LCKSPRNSLISMLKC 315  
 DB 301 LCKSPRNSLISMLKC 315

Search completed: February 4, 2004, 14:29:03  
 Job time : 44 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 4, 2004, 14:26:47 ; Search time 41 Seconds  
(without alignments)  
2152.536 Million cell updates/sec

Title: US-09-780-576-2

Perfect score: 1778

Sequence: 1 MQAVDNLTSAPGNTSLCTRD.....SODNRKKEQDGGDPNEETPM 342

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp\_archea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phage.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriapi.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1741	97.9	342	Q8HXH1	Q8hxh1 macaca fasc
2	1548.5	87.1	347	Q8BZV8	Q8bzx8 mus musculus
3	829	46.6	333	Q8BPV8	Q8bpv8 homo sapien
4	829	46.6	352	Q8IUT5	Q8iut5 homo sapien
5	823	46.3	333	Q8TDU7	Q8tdu7 homo sapien
6	794	44.7	337	Q9DBI2	Q9dbi2 mus musculus
7	792	44.5	337	Q8C412	Q8c412 mus musculus
8	789	44.4	337	Q8CAL2	Q8cal2 mus musculus
9	772	43.4	338	Q8IVT7	Q8ivt7 homo sapien
10	699.5	39.3	358	Q96JZ8	Q96jz8 homo sapien
11	694.5	39.1	358	Q9BZ21	Q9bz21 homo sapien
12	687	38.6	358	Q8C4Y7	Q8c4y7 mus musculus
13	685.5	38.6	359	Q99MT7	Q99mt7 mus musculus
14	559	31.4	228	Q9BE53	Q9be53 macaca fasc
15	553.5	31.1	269	Q9BXC2	Q9bxc2 homo sapien
16	487	27.4	319	Q8IV06	Q8iv06 homo sapien

17	483.5	27.2	319	11	Q8BY85	Q8by85 mus musculus
18	479.5	27.0	319	11	Q8BG55	Q8bg55 mus musculus
19	478.5	26.9	319	11	Q8CIF3	Q8cif3 mus musculus
20	465.5	26.2	317	11	Q8BEN1	Q8ben1 mus musculus
21	448	25.2	176	4	Q9BT61	Q9bt61 homo sapien
22	412.5	23.2	375	11	Q8BY11	Q8by11 mus musculus
23	388.5	21.9	342	6	Q9RTY5	Q9rtty5 bos taurus
24	387.5	21.8	342	6	Q9GK76	Q9gk76 capra hircu
25	368.5	20.7	296	6	Q9RTY6	Q9rtty6 canis famil
26	365	20.5	342	6	Q9XSD4	Q9xsd4 sus scrofa
27	364	20.5	341	11	Q8C017	Q8c017 mus musculus
28	356	20.0	374	13	Q57466	Q57466 meleagris g
29	351	19.7	344	11	Q8BMC0	Q8bmc0 mus musculus
30	343	19.3	359	13	Q9PVY7	Q9pvty7 anguilla an
31	338	19.0	359	6	Q9N0U1	Q9n0u1 ovis aries
32	336	18.9	309	11	Q8R528	Q8r528 mus musculus
33	327.5	18.4	339	4	Q8NS57	Q8ns57 homo sapien
34	322	18.1	359	11	Q9RPP3	Q9rpp3 cavia porce
35	321	18.1	359	6	Q9GLN9	Q9gln9 pan troglod
36	318.5	17.9	399	11	Q8R311	Q8r311 mus musculus
37	318	17.9	359	4	Q8TBK4	Q8tbk4 homo sapien
38	316.5	17.8	370	11	Q8BKK1	Q8bkk1 mus musculus
39	316	17.8	365	11	Q8BFP3	Q8bfp3 mus musculus
40	314	17.7	400	6	Q95M54	Q95m54 macaca fasc
41	313	17.6	370	11	Q8BLG2	Q8blg2 mus musculus
42	312.5	17.6	400	11	Q8CGM4	Q8cgm4 cavia porce
43	312	17.5	369	11	Q8BUB7	Q8bub7 mus musculus
44	311.5	17.5	355	6	Q8HZN5	Q8hzn5 macaca mula
45	309	17.4	358	13	Q9PUA0	Q9puao acipenser r

## ALIGNMENTS

### RESULT 1

Q8HXH1	PRELIMINARY;	PRT;	342 AA.
ID	Q8HXH1		
AC	Q8HXH1		
DT	01-MAR-2003 (TRENBLrel. 23, Created)		
DT	01-MAR-2003 (TRENBLrel. 23, Last sequence update)		
DT	01-MAR-2003 (TRENBLrel. 23, Last annotation update)		
DE	Hypothetical protein.		
OS	Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;		
OC	Cercopitheidae; Macaca.		
OX	NCBI_TaxID=9541;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISUE=Medulla oblongata;		
RA	Hashimoto K., Osada N., Hida M., Kusuda J., Sugano S.,		
RL	Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	TISUE=Medulla oblongata;		
RX	MEDLINE=21458551; PubMed=11574149;		
RA	Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirata M., Suto Y.,		
RA	Hirai M., Terao K., Suzuki Y., Sugano S., Hashimoto K.;		
RT	"Assignment of 118 novel cDNAs of cynomolgus monkey brain to human		
RT	chromosomes.";		
RL	Gene 275:31-37 (2001).		
DR	EMBL; AB037554; BAC11779.1; -		
KW	Hypothetical protein.		
SQ	SEQUENCE 342 AA; 39479 MW; 0869FDD0144A56FC CRC64;		

Query Match 97.9%; Score 1741; DB 6; Length 342;

Best Local Similarity 97.7%; Pred. No. 3.4e-140;

Matches 334; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 MQAVDNLTSAPGNTSLCTRDYKIQVLPFLYTVLFFVGLITNGLAMRIFPQIRSKNF 60

DB 1 MQAVDNLTSAPGNTSLCTRDYKIQVLPFLYTVLFFVGLITNGLAMRIFPQIRSKNF 60



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QY 61 IFKNTVVISDMLLTTPFKKILSDAKLGTGTLRTFVQVTSVIFFTMYISIFLGLITI 120
DB 61 IFKNTVVISDMLLTTPFKKILSDAKLGTGTLRTFVQVTSVIFFTMYISIFLGLITI 120
QY 121 DRYQKTRPFTKSNPKNLLGAKILSVVIMAFMFLSLPNMILNRPDRDNVKKCSFLKS 180
DB 121 DRYQKTRPFTKSNPKNLLGAKILSVVIMAFMFLSLPNMILNRPDRDNVKKCSFLKS 180
QY 181 EFGVLWHEIVNYICQVFWINFLVIVCYLITKELYRSVVRGVGKVPKKNVKKVFI 240
DB 181 EFGVLWHEIVNYICQVFWINFLVIVCYLITKELYRSVVRGVGKVPKKNVKKVFI 240
QY 241 IIAVFFICFVFFHARIPYTLISQTRDVFDCQTAENTLFYVKESTLWLTSLNACLDPIYFF 300
DB 241 IIAVFFICFVFFHARIPYTLISQTRDVFDCQTAENTLFYVKESTLWLTSLNACLDPIYFF 300
QY 301 LCKSFNLSMLKCPNSATSLSDNRKKEQDGDGDPNEETPM 342
DB 301 LCKSFNLSMLKCPNSATSLSDNRKKEQDGDGDPNEETPM 342

RESULT 2
Q8BZV8 PRELIMINARY; PRT; 347 AA.
ID Q8BZV8
AC Q8BZV8;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DE P2V12 platelet ADP receptor homolog.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Colon;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium;
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RL Nature 420:563-573(2002).
DR EMBL; AK033448; BAC28294.1; -.
SQ SEQUENCE 347 AA; 39430 MW; F114688377F225F1 CRC64;

Query Match 87.1%; Score 1548.5; DB 11; Length 347;
Best Local Similarity 88.4%; Pred. No. 7.9e-124;
Matches 298; Conservative 16; Mismatches 22; Indels 1; Gaps 1;

QY 6 NLTSAPGNTSLCTRDYKITQVLPFLYTLVFPVGLITNGLAMRFFQIRSKSNFIIFLKN 65
DB 12 NTFSPGNTSLCTRDYKITQVLPFLYTLVFPVGLITNGLAMRFFQIRSKSNFIIFLKN 71
QY 66 TWISDMLLTTPFKKILSDAKLGTGTLRTFVQVTSVIFFTMYISIFLGLITIDRYOK 125
DB 72 TWISDMLLTTPFKKILSDAKLGTGTLRTFVQVTSVIFFTMYISIFLGLITIDRYOK 131
QY 126 TTRPFTKSNPKNLLGAKILSVVIMAFMFLSLPNMILNRPDRDNVKKCSFLKSEGLV 185
DB 132 TTRPFTKSNPKNLLGAKILSVVIMAFMFLSLPNMILNRPDRDNVKKCSFLKSEGLV 191
QY 186 WHEIVNYICQVFWINFLVIVCYLITKELYRSVVRGVGKVPKKNVKKVFIIVAVF 245
DB 192 WHEIVNYICQVFWINFLVIVCYLITKELYRSVVRGVGKVPKKNVKKVFIIVAVF 251
QY 246 FLCFVFFHARIPYTLISQTRDVFDCQTAENTLFYVKESTLWLTSLNACLDPIYFFLCKSF 305
DB 252 FLCFVFFHARIPYTLISQTRDVFDCQTAENTLFYVKESTLWLTSLNACLDPIYFFLCKSF 311
QY 306 RNSLSMLKCPNSATSLSDNRKKEQDGDGDPNEETPM 342
DB 312 RNSLSMLKCSNS-TSTSGTNKKKGEGGEPSEETPM 347

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RESULT 3
Q8BZV8 PRELIMINARY; PRT; 333 AA.
ID Q8BZV8
AC Q8BZV8;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Putative G-protein-coupled receptor PKSG77 (G-protein coupled receptor
DE GPR86) (G-protein-coupled receptor) (G protein-coupled receptor
DE GPR86).
GN PKSG77 OR GPR86 OR GPR94.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA Wang Y.; Gong L.;
RT "Molecular cloning of PKSG77, a novel gene encoding a putative G-
RT protein-coupled receptor."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21172992; PubMed=11273702;
RA Wittenberger T.; Schaller H.C.; Hellebrand S.;
RT "An expressed sequence tag (est) data mining strategy succeeding in
RT the discovery of new G-protein coupled receptors."
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21458557; PubMed=11574155;
RA Lee D.K.; Nguyen T.; Lynch K.R.; Cheng R.; Vanti W.B.; Arkhitko O.;
RA Lewis T.; Evans J.F.; George S.R.; O'Dowd B.F.;
RT "Discovery and mapping of ten novel G protein-coupled receptor
RT genes."
RL Gene 275:83-91(2001).
RN [4]
RP SEQUENCE FROM N.A.
RX PubMed=11546776;
RA Communi D.; Gonzalez N.S.; Dethieux M.; Brezillon S.; Lannoy V.;
RA Farmentier M.; Boeynaems J.M.;
RT "Identification of a Novel Human ADP Receptor Coupled to Gi."
RL J. Biol. Chem. 276:41479-41485(2001).
DR EMBL; AF345565; AKK29068.1; -
DR EMBL; AF293368; AKK01864.1; -
DR EMBL; AF411113; AAL26484.1; -
DR EMBL; AF406692; AAL01038.1; -
DR Genes; HGNC:4537; GPR86.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 333 AA; 38440 MW; F234ABB50016DF34 CRC64;

Query Match 46.6%; Score 829; DB 4; Length 333;
Best Local Similarity 49.1%; Pred. No. 1.1e-62;
Matches 155; Conservative 57; Mismatches 102; Indels 2; Gaps 1;

QY 17 CTRDYKITQVLPFLYTLVFPVGLITNGLAMRFFQIRSKSNFIIFLKNVVISDMLLT 76
DB 15 CPEDTRIVQLVFPALYTVVFLTGILNTALWVFIHPSSTFIYLNKTLVADLIMTL 74
QY 77 FFPKILSDAKLGTGTLRTFVQVTSVIFFTMYISIFLGLITIDRYOKTRPFTKSNPK 136
DB 75 LFPKILSDSLHAPQLARAFVCFPSVIFVETVYVGLGLIADRFILKIRPLRNIFLK 134
QY 137 NLGAKILSVVIMAFMFLSLPNMILNRPDRDNVKKCSFLKSEGLVWHEIVNYICQV 196
DB 135 KPVFAKTVSIFWFFLFFISLPNLSNKEATPSVKKCASLKGPLGLKWHQWNNICQF 194

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QY 197 IFWINFLIVVYTLITKELYRSYVTRGVGKVRKKNVKKVFIILIAVFFICVPPHFAR 256
DB 195 IFWTVFILMVFYVIAKVYDSYRKSCKDRKNKKLEGKVFVWVAVFVCFAPHFAR 254
QY 257 IPYTLSDTRDVFDCATNTLFFVKESTLWLTSLNACLDPFYFVFLCKSPNSLSMLKCP 316
DB 255 VPYTHSQNNKTDCLQNLQFIKATETTLFLAANTNLCMDPLIYFLCKFKTEKLPQM-Q 312
QY 317 NSATSLSDNRKKEQD 332
DB 313 RKTASSQENHSSQTD 328

RESULT 4
Q81U75
ID Q81U75 PRELIMINARY; PRT; 352 AA.
AC Q81U75;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
FN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (DSC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC041116; AAH41116.1; -
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 352 AA; 40586 MW; BCABBE1E405872B CRC64;

Query Match 46.6%; Score 829; DB 4; Length 352;
Best Local Similarity 49.1%; Pred. No. 1.2e-62;
Matches 155; Conservative 57; Mismatches 102; Indels 2; Gaps 1;

QY 17 CTRDYKIQVLPFLLYTVLFFVGLITNGLAMRIFFOIRSKSNFIIFLKNVTISDLMLT 76
DB 34 CPROTRIVQLVFPALYTVVLTGILLNTLALWVFPVHPSSSTFIYILKNTLVADLIMTL 93
QY 77 PPFKILSDAKLGTGRLTFVQVTSVIFYFTMYISISFLGLITIDRYOKTRPFKTSNPK 136
DB 94 LPFKILSDSLAPQLRAFVCRFSVIFYETMYGVILGLIAFDRLFKIRPLRNIFLK 153
QY 137 NLIGAKILSVIWMFLLSLPNMILTRQDRDNKVKCKSEFLGVWHEIVNYICQV 196
DB 154 KPVEAKTVSIFWFLFISLPNLSLKEATPSVKKCASLKGPLGLKWHQWNNICQF 213
QY 197 IFWINFLIVVYTLITKELYRSYVTRGVGKVRKKNVKKVFIILIAVFFICVPPHFAR 256
DB 214 IFWTVFILMVFYVIAKVYDSYRKSCKDRKNKKLEGKVFVWVAVFVCFAPHFAR 273
QY 257 IPYTLSDTRDVFDCATNTLFFVKESTLWLTSLNACLDPFYFVFLCKSPNSLSMLKCP 316
DB 274 VPYTHSQNNKTDCLQNLQFIKATETTLFLAANTNLCMDPLIYFLCKFKTEKLPQM-Q 331
QY 317 NSATSLSDNRKKEQD 332
DB 332 RKTASSQENHSSQTD 347

RESULT 5
Q8TDU7
ID Q8TDU7 PRELIMINARY; PRT; 333 AA.
AC Q8TDU7;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Putative G-protein coupled receptor.
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GN GPCR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
FN [1]
RP SEQUENCE FROM N.A.
RA Takada S., Kadowaki S., Haga T., Takaeu H., Mitaku S.;
RT Identification of G protein-coupled receptor genes from the human
RL genome sequence.
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB083597; BAB9310.1; -
DR InterPro; IPR00276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 333 AA; 38409 MW; 3F88E7EAC9F5428F CRC64;

Query Match 46.3%; Score 823; DB 4; Length 333;
Best Local Similarity 48.7%; Pred. No. 3.6e-62;
Matches 154; Conservative 57; Mismatches 103; Indels 2; Gaps 1;

QY 17 CTRDYKIQVLPFLLYTVLFFVGLITNGLAMRIFFOIRSKSNFIIFLKNVTISDLMLT 76
DB 15 CPROTRIVQLVFPALYTVVLTGILLNTLALWVFPVHPSSSTFIYILKNTLVADLIMTL 74
QY 77 PPFKILSDAKLGTGRLTFVQVTSVIFYFTMYISISFLGLITIDRYOKTRPFKTSNPK 136
DB 75 LPFKILSDSLAPQLRAFVCRFSVIFYETMYGVILGLIAFDRLFKIRPLRNIFLK 134
QY 137 NLIGAKILSVIWMFLLSLPNMILTRQDRDNKVKCKSEFLGVWHEIVNYICQV 196
DB 135 KPVEAKTVSIFWFLFISLPNLSLKEATPSVKKCASLKGPLGLKWHQWNNICQF 194
QY 197 IFWINFLIVVYTLITKELYRSYVTRGVGKVRKKNVKKVFIILIAVFFICVPPHFAR 256
DB 195 IFWTVFILMVFYVIAKVYDSYRKSCKDRKNKKLEGKVFVWVAVFVCFAPHFAR 254
QY 257 IPYTLSDTRDVFDCATNTLFFVKESTLWLTSLNACLDPFYFVFLCKSPNSLSMLKCP 316
DB 255 VPYTHSQNNKTDCLQNLQFIKATETTLFLAANTNLCMDPLIYFLCKFKTEKLPQM-Q 312
QY 317 NSATSLSDNRKKEQD 332
DB 313 RKTASSQENHSSQTD 328

RESULT 6
Q9D8I2
ID Q9D8I2 PRELIMINARY; PRT; 337 AA.
AC Q9D8I2;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE 2010001106Rik protein.
GN GPR86 OR 2010001106RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
FN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Small intestine;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yananaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Giesi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
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RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barah G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Guscinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohnauki S.,  
RA Hayashizaki Y.,  
RT "Functional annotation of a full-length mouse cDNA collection."  
RL Nature 409:695-699(2001).  
DR EMBL; AK008013; BAB25409.1; -  
DR MGD; MGI:1921441; Gpr86.  
DR InterPro; IPR000276; GPCR\_Rhodopsin.  
DR InterPro; IPR005466; UDG\_receptor.  
DR Pfam; PF00001; 7tm\_1; 1.  
DR PRINTS; PR00237; GPCR\_Rhodopsin.  
DR PRINTS; PR01655; UDG\_LUCOSER.  
DR PROSITE; PS00237; G\_PROTEIN\_RECP FL 1; 1.  
DR PROSITE; PS0262; G\_PROTEIN\_RECP FL 2; 1.  
SQ SEQUENCE 337 AA; 38693 MW; 2C1A76FB893D5EA CRC64;

Query Match 44.7%; Score 794; DB 11; Length 337;  
Best Local Similarity 45.9%; Pred. No. 1.1e-59;  
Matches 151; Conservative 63; Mismatches 111; Indels 4; Gaps 3;

QY 6 NLTSAPG--NTSLCTRDYKIQVLFPPLLYTVLFFVGLITNGLAMRIFQIRKSNFIIFL 63  
Db 6 NTTGMOGFKSERCPDRTRMTQLLPVLYTVVFLAGILLNTVALWVPHIPSNSTFIIVL 65

QY 64 KNTVISDLMLITPFPFKILSDAKLGTGRLPFCQVTSVIFFTMYISIFLGLITIDRY 123  
Db 66 KNTLVADLIMALMFPFKILSDHAPLQWLRGFCVCTLSVWFYETMYGIMMGLIAFDRF 125

QY 124 OKTTRPFTSNPKNLLGAKILSVIWFAPFLLSLPNMILTNRQPRDKNVKCKSLKSEFG 183  
Db 126 LKIIMPFRTFKTAPAKTIVSISWSLMPFISLPNML-NKEATPSSVKKCSLKSPLG 184

QY 184 LWHEIVNYICQVIFWIFNFIIVCYTLITKELRSYVRGVGKVRKKNVKVFIILIA 243  
Db 185 LWWHQVSHSTCOLIFWAVFIIMLLFYAVITKKVNSYRKFRSKDS-RHKLELVKVFVIMA 243

QY 244 VFFICFVFPFHARIPYTLISQTRDVFDCVAENTLFVVKESTLWTLNACLDPFTFYFLCK 303  
Db 244 VFFVCFAPLHFVRIPYTSQTNKTDCELENQLFIAKEATLFLATTNICMDPLIYILCK 303

QY 304 SFRNSLISMLKCPNSATLSQDNKKKED 332  
Db 304 KFTQKPCVRWGKARTAGSSEHSSQTD 332

RESULT 8  
Q8C412 PRELIMINARY; PRT; 337 AA.

ID Q8C412  
AC Q8C412;  
DT 01-MAR-2003 (TREMELrel. 23, Created)  
DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)  
DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)  
DE G protein-coupled receptor 68 homolog.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Hypothalamus;  
RX MEDLINE=22354683; Pubmed=12466851;  
RA The FANTOM Consortium,  
RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RL Nature 420:563-573(2002).  
DR EMBL; AK038560; BAC30043.1;  
SQ SEQUENCE 337 AA; 38755 MW; 70E9AA7B98089B0A CRC64;

Query Match 44.4%; Score 789; DB 11; Length 337;  
Best Local Similarity 45.6%; Pred. No. 2.9e-59;  
Matches 150; Conservative 63; Mismatches 112; Indels 4; Gaps 3;

QY 6 NLTSAPG--NTSLCTRDYKIQVLFPPLLYTVLFFVGLITNGLAMRIFQIRKSNFIIFL 63  
Db 6 NTTGMOGFKSERCPDRTRMTQLLPVLYTVVFLAGILLNTVALWVPHIPSNSTFIIVL 65

QY 64 KNTVISDLMLITPFPFKILSDAKLGTGRLPFCQVTSVIFFTMYISIFLGLITIDRY 123  
Db 66 KNTLVADLIMALMFPFKILSDHAPLQWLRGFCVCTLSVWFYETMYGIMMGLIAFDRF 125

QY 124 OKTTRPFTSNPKNLLGAKILSVIWFAPFLLSLPNMILTNRQPRDKNVKCKSLKSEFG 183  
Db 126 LKIIMPFRTFKTAPAKTIVSISWSLMPFISLPNML-NKEATPSSVKKCSLKSPLG 184

QY 184 LWHEIVNYICQVIFWIFNFIIVCYTLITKELRSYVRGVGKVRKKNVKVFIILIA 243  
Db 185 LWWHQVSHSTCOLIFWAVFIIMLLFYAVITKKVNSYRKFRSKDS-RHKLELVKVFVIMA 243

QY 244 VFFICFVFPFHARIPYTLISQTRDVFDCVAENTLFVVKESTLWTLNACLDPFTFYFLCK 303  
Db 244 VFFVCFAPLHFVRIPYTSQTNKTDCELENQLFIAKEATLFLATTNICMDPLIYILCK 303

QY 304 SFRNSLISMLKCPNSATLSQDNKKKED 332  
Db 304 KFTQKPCVRWGKARTAGSSEHSSQTD 332

RESULT 7  
Q8C412 PRELIMINARY; PRT; 337 AA.

ID Q8C412  
AC Q8C412;  
DT 01-MAR-2003 (TREMELrel. 23, Created)  
DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)  
DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)  
DE G protein-coupled receptor 68 homolog.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Hippocampus;  
RX MEDLINE=22354683; Pubmed=12466851;  
RA The FANTOM Consortium,  
RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RL Nature 420:563-573(2002)."

Db 185 LWHEQVSHSTCOFIWAVFIMLLFYAVITKTVNSYKFRSKDS-RHKELEVRVFVMA 243  
QY 244 VFICVFPFHARIPYTLSTQTRDVFDCATNTLFFVYKESLTLWLSNACLDPIIYFLCK 303  
Db 244 VFCVFPFHARIPYTLSTQTRDVFDCATNTLFFVYKESLTLWLSNACLDPIIYFLCK 303  
QY 304 SFRNSLSMLKCPNSATSLSDNRKKEQD 332  
Db 304 KFTQKQPCVRWGKARTAGSSSEHSSQTD 332

RESULT 9

Q8IYT7 PRELIMINARY; PRT; 338 AA.  
AC Q8IYT7;  
DT 01-MAR-2003 (TremBLrel. 23, Created)  
DT 01-MAR-2003 (TremBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)  
DE G protein-coupled receptor 105.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Testis;  
RA Strausberg R.;  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
KW Receptor.  
SQ SEQUENCE 338 AA; 38972 MW; 8871408E2F392DEB CRC64;

Query Match 43.4%; Score 772; DB 4; Length 338;

Best Local Similarity 47.5%; Pred. No. 8e-58;

Matches 149; Conservative 60; Mismatches 105; Indels 0; Gaps 0;

QY 6 NLTSAPGNTSLCTRDYKITQVLPFLYTLVLFVGLITNGLAMRFFOIRKSNFIPLKN 65  
Db 3 NSTSTQPDSCSNLITQIIPVLCWVFIAGILANGSGWIFFVPSSEFIYLVKN 62  
QY 66 TVISDLMLITFPFKILSDAKLGTGPTRTVCQVTSVIFFTMYISIFGLITIDRYQK 125  
Db 63 IVIADFVMSLTFPPEKILDSGLGQWLNQVFCRVSAVLFFYNNVYSIVFFGLISDFRYK 122  
QY 126 TTRPFTSNPNKLGAKILSVIWAFFLLSLPNMLTNPQPRDKNVKCSFLKSEPLV 185  
Db 123 IVKPLWTSFIOVSYSKLLSVIWMMLLLAVPNIITNQSREVTQIKIELKSELGRK 182  
QY 186 WHEIVNYICQVIFWIFNLIVICVTLITKELYSYVTRGVKVPKKNVVFIIIAVF 245  
Db 183 WHKASNYIFVAIFWIFVLLIVFTAITKTFKSHLKSRRNSTSVKKSRRNIFSIIVVF 242  
QY 246 FICVFPFHARIPYTLSTQTRDVFDCATNTLFFVYKESLTLWLSNACLDPIIYFLCKSF 305  
Db 243 FVCVFPFHARIPYTLSTQTRDVFDCATNTLFFVYKESLTLWLSNACLDPIIYFLCKQFP 302  
QY 306 RNSLSMLKCPNSA 319  
Db 303 REILCKLHILPKA 316

RESULT 10

Q96JZ8 PRELIMINARY; PRT; 358 AA.  
AC Q96JZ8;  
DT 01-DEC-2001 (TremBLrel. 19, Created)  
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)  
DE Hypothetical protein FLU14878.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Placenta;  
RA Isoai T., Ota T., Hayashi K., Sugiyama T., Otauki T., Suzuki Y.,  
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,  
RA Wagatsuma M., Hosoi T., Kaku Y., Kudoira H., Kondo H., Sugawara M.,  
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,  
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,  
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,  
RA Ninomiya K., Iwayanagi T.,  
RA NEDO human cDNA sequencing project.  
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
CC -|- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
CC -|- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
DR EMBL; AK027784; BAB55366.1; -  
DR Genew; HGNC:4538; GPR87.  
DR InterPro; IPR000276; GPCR\_Rhodpsn.  
DR Pfam; PF00001; 7tm.1; 1.  
DR PRINTS; PRO0237; GPCRHHODOPSN.  
DR PROSITE; PS00337; G-PROTEIN RECEPTOR FL1; 1.  
DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL2; 1.  
KW Hypothetical protein; G-protein coupled receptor; Receptor;  
KW Transmembrane.  
SQ SEQUENCE 358 AA; 41462 MW; 7822700C8E3CC7E9 CRC64;

Query Match 39.3%; Score 699.5; DB 4; Length 358;

Best Local Similarity 42.6%; Pred. No. 1.2e-51;

Matches 140; Conservative 67; Mismatches 113; Indels 9; Gaps 5;

QY 6 NLTSAPGNTSLCTRDYKITQVLPFLYTLVLFVGLITNGLAMRFFOIRKSNFIPLK 64  
Db 25 NRSDFGPKNTL--HNEFDIVLPVLIIFVASILLNGLAVVIFHIRKTSFIFLK 81  
QY 65 NTVISDLMLITFPFKILSDAKLGTGPTRTVCQVTSVIFFTMYISIFGLITIDRYQ 124  
Db 82 NTIWDADLMLITFPFKILSDAKLGTGPTRTVCQVTSVIFFTMYISIFGLITIDRYL 141  
QY 125 KTRPFTSNPNKLGAKILSVIWAFFLLSLPNMLTNPQPRDKNVKCSFLKSEPL 184  
Db 142 KVKFPGSRMYNITFTKVLSCVWVNAVLSLNPILITNGQPTEDNHDCKSLKSLGV 201  
QY 185 WHEIVNYICQVIFWIFNLIVICVTLITKELYSYVTRGVKVPK-KVNVKVFIIIA 243  
Db 202 KWHATAVTVNSCLFVAVLVILGICVYALSRYIHKS--SRQFISQSSRRKKNQIRVVA 259  
QY 244 VFICVFPFHARIPYTLSTQTRDVFDCATNTLFFVYKESLTLWLSNACLDPIIYFLCK 303  
Db 260 VFTCTPLPHLCRIPFTFTHLDRLLDESAQKILYICKETLFLSACNVCLDPIIYFMC 319  
QY 304 SFRNSLS--SMLKCPNSATSLSDNRKKE 330  
Db 320 SPSRRLFKKSNIRTSSESIRSLQSVRSE 348

RESULT 11

Q9BY21 PRELIMINARY; PRT; 358 AA.  
AC Q9BY21;  
DT 01-JUN-2001 (TremBLrel. 17, Created)  
DT 01-JUN-2001 (TremBLrel. 17, Last sequence update)  
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)  
DE Orphan G protein-coupled receptor 87.  
GN GPR87 OR GPR95.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21172992; PubMed=11273702;  
RA Wittenberger T., Schaller H.C., Hellebrand S.;  
RT "An expressed sequence tag (est) data mining strategy succeeding in



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Db 86 VADLIMLTTPFRIVRDAGFGPWYFEBILCRYTSVLFYANNYTSIVPLGLISVDRYLKV 145
Qy 128 RPFKTSNPKLLGAKILSVIWAFLSLPMLNLTNRQPRDKVKKCSFLKSEFGLVWH 187
Db 146 KFGDSSWISITFTKVLSCVWVIMAILSPNLTNGOPTKENIHDCMKLSPFLGAKWH 205
Qy 188 EIVNYICQVIFWFLNFIIVCYTLITKELYSYVTRGVGKPRK-KVNVKVFIIIAVFF 246
Db 206 MAVTVDSCLFVAVLVILGCIYASRYHKS--SRQFISQSRKKHNSIRVVAVVF 263
Qy 247 ICFVFFHFAIPVTLSTDRVFDCTAENTLFYKVESTLMTLSNACLDPFIIFFLCKSFR 306
Db 264 TCELVFHLCPFFFSNLDRLDESAAKILYCKEMLTFLSACNVCLDPIIYFMMCKSFS 323
Qy 307 NSLI--SMLKCPNSATSLSDNRKKE 330
Db 324 RRLFCKSNIRTSIESIRLSQVRSE 349

RESULT 14
Q9BE53 PRELIMINARY; PRT; 228 AA.
ID AC Q9BE53
DC Q9BE53; 2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE "Isolation of full-length cDNA clones from macaque brain CDNA libraries."
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciae;
OC Cercopitheciae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Frontal cortex;
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA Suzuki Y., Sugano S., Hashimoto K.;
RT "Isolation of full-length cDNA clones from macaque brain CDNA libraries."
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB056816; BAB39342.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCR_Rhodpsn.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
SQ SEQUENCE 228 AA; 26356 MW; 47907F5DBEDD22C CRC64;

Query Match 31.4%; Score 559; DB 6; Length 228;
Best Local Similarity 46.7%; Pred. No. 7.1e-40;
Matches 105; Conservative 40; Mismatches 78; Indels 2; Gaps 1;

Qy 108 MYISIFLGLITIDRYOKTTTPKTSNPKLLGAKILSVIWAFLSLPMLNLTNRQP 167
Db 1 MYGVIVLGLIADRFUKIIRPLNLTFTKTVFVLMVYVVIKAYVDSYKSKSD 60
Qy 168 RDNKVKCSFLKSEFGLVWHIEVNYICQVIFWFLNFIIVCYTLITKELYSYVTRGVG 227
Db 61 TESSVKKCASLKGPLGKHLQVNNISQPIFTWVFLMLVYVVIKAYVDSYKSKSD 120
Qy 228 KVPKKNVNVKVFIIIAVFFICFPFHFAIPVTLSTDRVFDCTAENTLFYKVESTLMT 287
Db 121 RKNKLEGVVYVAVVAVVFVCFAPFFHTRVPTYSQTNKNTDRLQNLFIKETTFLA 180
Qy 288 SLNACLDPFIYFLCKSFRNSLI-SMLKCPNSATSLSDNRKKEQD 332
Db 181 ATNLCMDPLIYFLCKKFTKLCPCMRGRKTIAS--SQENQSQTD 223

RESULT 15
Q9BXC2 PRELIMINARY; PRT; 269 AA.
ID AC Q9BXC2
AC Q9BXC2;
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DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative G-protein-coupled receptor FKG78 (G protein-coupled receptor 87).
GN FKG78.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA Wang Y.-G., Gong L.;
RT "Identification of FKG78, a novel gene encoding a putative G-protein-coupled receptor."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AP345566; AAK29069.1; -
DR EMBL; BC009540; AAH09540.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCR_Rhodpsn.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 269 AA; 31443 MW; 1E7D498EE20717F6 CRC64;

Query Match 31.1%; Score 553.5; DB 4; Length 269;
Best Local Similarity 42.5%; Pred. No. 2.4e-39;
Matches 111; Conservative 50; Mismatches 95; Indels 5; Gaps 3;

Qy 73 MLITFPFKILSDAKLGHCPLETFVQCVTSTVFTWYISIFLGLITIDRYOKTTPEPKT 132
Db 1 MTLTFPRIVHDAGFGPWYFEBILCRYTSVLFYANNYTSIVPLGLISIDRYLVKVFEGD 60
Qy 133 SNPKLLGAKILSVIWAFLSLPMLNLTNRQPRDKVKKCSFLKSEFGLVWHIEVNY 192
Db 61 SRMYSITFTKVLSCVWVIMAILSPNLTNGOPTKENIHDCMKLSPFLGAKWHATVY 120
Qy 193 ICQVIFWFLNFIIVCYTLITKELYSYVTRGVGKPRK-KVNVKVFIIIAVFFICFVP 251
Db 121 VNSCLFVAVLVILGCIYASRYHKS--SRQFISQSRKKHNSIRVVAVVFVTCFLP 178
Qy 252 FHFARIPVTLSTDRVFDCTAENTLFYKVESTLMTLSNACLDPFIYFLCKSFRNSLI- 310
Db 179 YHLCRIPTFTSHLDRLDESAAKILYCKEITFLSACNVCLDPIIYFPMCRSFRLEFK 238
Qy 311 -SMLKCPNSATSLSDNRKKE 330
Db 239 KSNIRTSIESIRLSQVRSE 259

Search completed: February 4, 2004, 14:30:26
Job time : 42 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 4, 2004, 14:27:22 ; Search time 20 Seconds  
(without alignments)  
1644.484 Million cell updates/sec

Title: US-09-780-576-2

Perfect score: 1778

Sequence: 1 MQAVDNLTSAPGNTSLCTRD.....SQDNKKKQDGGDPNEETPM 342

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 76:\*\*  
1: PIR1:\*\*  
2: PIR2:\*\*  
3: PIR3:\*\*  
4: PIR4:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	394	22.2	342	2 A40191
2	392.5	22.1	342	2 S13638
3	379.5	21.3	361	2 A45580
4	366	20.6	341	2 S63866
5	362	20.4	341	2 S43252
6	357.5	20.1	308	2 I50241
7	339	19.1	359	2 S15403
8	338	19.0	344	2 T09508
9	329	18.5	359	2 I39418
10	326	18.3	359	2 S44425
11	325.5	18.3	399	2 I48705
12	325	18.3	359	2 A48857
13	321	18.1	359	2 J41104
14	321	18.1	370	2 JC5549
15	319	17.9	359	2 A42656
16	319	17.9	359	2 JC2134
17	318	17.9	359	2 JC1194
18	318	17.9	359	2 JH0821
19	317.5	17.9	365	2 S68208
20	317.5	17.9	398	2 I56517
21	314.5	17.7	398	2 I56504
22	314	17.7	359	2 JQ1516
23	313.5	17.6	380	2 I38435
24	310.5	17.5	362	2 JN0694
25	309	17.4	392	2 S65893
26	309	17.4	400	2 I56533
27	306	17.2	397	2 S66518
28	304.5	17.1	398	2 A57510
29	299	16.8	380	2 JC2434

30 298.5 16.8 365 2 S68679  
31 298 380 2 A48227  
32 297.5 16.7 359 2 I51372  
33 297.5 16.7 360 2 A53611  
34 297 16.7 380 2 A55259  
35 296.5 16.7 420 2 I51667  
36 296 380 2 S36143  
37 295 16.6 380 2 JC2338  
38 292.5 16.5 362 2 S33733  
39 291.5 16.4 373 2 A47556  
40 290.5 16.3 352 2 A45747  
41 284.5 16.0 333 2 I38974  
42 282.5 15.9 352 2 G00048  
43 282 15.9 352 2 A43113  
44 282 15.9 355 2 JQ1231  
45 281.5 15.8 353 2 S28787

G protein-coupled  
kappa opioid recep  
angiotensin II rec  
interleukin-8 rece  
kappa opioid recep  
thrombin receptor  
kappa opioid recep  
kappa opioid recep  
G protein-coupled  
ATP receptor P2u -  
neuropeptide Y/pep  
G protein-coupled  
fusin (LESTRA) - c  
chemokine (C-C) re  
interleukin-8 rece  
neuropeptide Y/pep

## ALIGNMENTS

RESULT 1  
A40191  
platelet-activating factor receptor - human  
C:Species: Homo sapiens (man)  
C>Date: 28-Aug-1992 #sequence revision 28-Aug-1992 #text change 20-Jun-2000  
C/Accession: A40191; JH0479; A41079; JCI359; A42831; I51923  
R/Kunz, D.; Gerard, N.P.; Gerard, C.  
J. Biol. Chem. 267, 9101-9106, 1992  
A/Title: The human leukocyte platelet-activating factor receptor. cDNA cloning, cell su  
A/Reference number: A40191; MUID:92250505; PMID:1374385  
A/Accession: A40191  
A/Molecule type: mRNA  
A/Residues: 1-342 <KUN>  
A/Cross-references: GB:M76674; NID:G456293; PIDN:AAA60002.1; PID:G456294  
R.Ye, R.D.; Prossnitz, E.R.; Zou, A.; Cochran, C.G.  
Biochem. Biophys. Res. Commun. 180, 105-111, 1991  
A/Title: Characterization of a human CDNA that encodes a functional receptor for platelet  
A/Reference number: JH0479; MUID:92028922; PMID:1656963  
A/Accession: JH0479  
A/Molecule type: mRNA  
A/Residues: 1-342 <YER>  
A/Cross-references: GB:M80436; NID:G189537; PIDN:AAA60001.1; PID:G189538  
R.Nakamura, M.; Honda, Z.; Izumi, T.; Sakanaka, C.; Mutoh, H.; Minami, M.; Bito, H.; Se  
J. Biol. Chem. 266, 20400-20405, 1991  
A/Title: Molecular cloning and expression of platelet-activating factor receptor from hu  
A/Reference number: A41079; MUID:92041873; PMID:1657923  
A/Accession: A41079  
A/Status: not compared with conceptual translation  
A/Molecule type: mRNA  
A/Residues: 1-342 <NAK>  
A/Cross-references: GB:D10202; NID:G219975; PIDN:BAA01050.1; PID:G219976  
R.Sugimoto, T.; Tsuchimoto, H.; McGregor, C.G.A.; Mutoh, H.; Shimizu, T.; Kurachi, Y.  
Biochem. Biophys. Res. Commun. 189, 617-624, 1992  
A/Title: Molecular cloning and characterization of the platelet-activating factor recep  
A/Reference number: JCI359; MUID:93112021; PMID:1281995  
A/Accession: JCI359  
A/Molecule type: mRNA  
A/Residues: 1-315, 'N', 317-342 <SUG>  
A/Experimental source: heart  
A/Note: the authors translated the codon AAT for residue 316 as Lys  
Riseyried, C.B.; Schweickart, V.L.; Godiska, R.; Gray, P.W.  
Genomics 13, 832-834, 1992  
A/Title: The human platelet-activating factor receptor gene (PTAFR) contains no introns  
A/Reference number: A42831; MUID:92347886; PMID:1322356  
A/Accession: A42831  
A/Molecule type: DNA  
A/Residues: 1-226, 'TG', 229-342 <SEV>  
A/Cross-references: GB:M8177; NID:G190697; PIDN:AAA60214.1; PID:G190698  
A/Note: sequence extracted from NCBI backbone (NCBIN:109813, NCBIF:109814)  
R.Chase, P.B.; Halonen, M.; Regan, J.W.  
Am. J. Respir. Cell Mol. Biol. 8, 240-244, 1993



A>Title: Cloning of a human platelet-activating factor receptor gene: evidence for an intron  
A/Reference number: I51923; MUID:93192035; PMID:8383507

A/Accession: I51923

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-342 <RES>

A/Cross-references: GB:S56396; NID:g298580; PIDN:AAB25755.1; PID:g298581

C/Genetics:

A/Genes: GDB:PTAFR

A/Cross-references: GDB:I28806; OMIM:173393

A/Map position: lp35-lp34.3

C/Superfamily: ATP receptor P2u

C/Keywords: G protein-coupled receptor; transmembrane protein

P:17-38/Domain: transmembrane #status predicted <TRI>

P:54-75/Domain: transmembrane #status predicted <VII>

P:92-113/Domain: transmembrane #status predicted <III>

P:134-155/Domain: transmembrane #status predicted <TRV>

P:184-205/Domain: transmembrane #status predicted <TRV>

P:233-253/Domain: transmembrane #status predicted <TVI>

P:277-297/Domain: transmembrane #status predicted <VII>

Query Match 22.2%; Score 394; DB 2; Length 342;

Best Local Similarity 32.6%; Pred. No. 1.5e-26;

Matches 107; Conservative 61; Mismatches 134; Indels 26; Gaps 10;

QY 11 PNTSLCTRDYKITQVLPFLYTLVFLVGLITNGLAMRIFFQIR--SKSNFI-IFLKNTV 67

DB 3 PHDSHMDSEPRYT-LFPIVYSIFVLGVANGYLVWFAVLPCKKFEIKFIWVNT 60

QY 68 ISDLMLITPFFKLSDAKLTGTRFVQCVTSVIFYFMYISISLGLITIDRYOKIT 127

DB 61 MADLFLITFLWVYQNGNWILPKLNCVAGCLFFINTYCSVAPLGVITNRFQAVT 120

QY 128 RPFKTSNPKNLGAKILSVIWIW----AFMFLSLPNNMILTNQPRDK---NVYKCSFLK 179

DB 121 RPIKTAQANTKRGISLSLVWALVGAASVFLIDS---TNTVPDSAGSGNTRC-FEH 176

QY 180 SEGLVWHEIYNYCCQVIFWNLIVIVCYTLITKELYRVSRTGVRGKVPKKNVQVP 239

DB 177 YKGSVPVLIITHIFVSFFVLFLILFCNLVILITLQMPVQOQNAEYKRRALNW-VC 235

QY 240 IIAVFFICFPVFFHARIPYTLSTQTRVDFCTAENTLFFYKESLWLTSLNACLDPEIYF 299

DB 236 TVLAVFLICFPVHHVQLPWLAEL-GFQDSKPHQAINDAHQVTLCLSTNCVLDPIYC 294

QY 300 FLCKSFRN-----SLISMLKCPNSAT 320

DB 295 FLTKKFKHLTEKFYSMRSSKCRATT 322

RESULT 2

S13638

C/Species: Cavia porcellus (guinea pig)

C/Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 08-Oct-1999

A/Accession: S13638

R/Honda, Z.; Nakamura, M.; Miki, I.; Minami, M.; Watanabe, T.; Seyama, Y.; Okado, H.; To

Nature 349, 342-346, 1991

A>Title: Cloning by functional expression of platelet-activating factor receptor from gu

A/Reference number: S13638; MUID:91101726; PMID:1846231

A/Accession: S13638

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-342 <CON>

A/Cross-references: GB:X56736; NID:g49442; PIDN:CAA40060.1; PID:g49443

A/Note: the species of guinea pig is not identified; in GenBank entry CCPAFREC, release

C/Superfamily: ATP receptor P2u

Query Match

Best Local Similarity 22.1%; Score 392.5; DB 2; Length 342;

Matches 103; Conservative 66; Mismatches 146; Indels 21; Gaps 9;

QY 20 DYKITQVLPFLYTLVFLVGLITNGLAMRIFFQI--RSKSNFI-IFLKNTVISDLMLIT 76

DB 10 DSEPRYLFPFIVISIIIFVLGLIANGYVWFAVLPSPKLNKNEIKIFWVNTVADLLFLIT 69

QY 77 PPFKILSDAKLTGTRFVQCVTSVIFYFMYISISLGLITIDRYOKTRPFTSNPK 136

DB 70 LPLWIVYSNGQNWFLPKFLCNLAGCLFFINTYCSVAFGLGVITVNRQAVKYPDKTAQAT 129

QY 137 NLGAKILSVIWIW----AFMFLSLPNNMILTNQPRDKVKKCSFLKSEFG---LVWH 187

DB 130 TRKGIALSLVIVAIIVAAASYFLVMDSTNVSNKAGSGNITRC-FEHYKSGKPVLIH 188

QY 188 EIVNYICQVI-FWINFLIVIVCYTLITKELYRVSRTGVRGKVPKKNVKKVFIIVAVFF 246

DB 189 -----ICVLGFFVFLILFCNLVILITLRLQPVQOQNAEV-RRRALWVCTVLAVFV 242

QY 247 ICFVPPHARIPYTLSTQTRVDFCTAENTLFFYKESLWLTSLNACLDPEIYFELCKSER 306

DB 243 ICFVPHHVVQLPWLAEL-GMWPSNSHOAINDAHQVTLCLSTNCVLDPIYICFLTCKFR 301

QY 307 NSLISMLKCPNSATSLSQDNRKKEQDGDGDPNEETPM 342

DB 302 KHLSEKLNIMSGSKSRVTTDTGTETMAIPINHTFV 337

RESULT 3

B45680

G protein-coupled peptide receptor EBI 2 - human

C/Species: Homo sapiens (man)

C/Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Jul-2000

A/Accession: B45680

R/Birkenbach, M.; Josefsen, K.; Yamamachi, R.; Lenoir, G.; Kieff, E.

J. Virol. 67, 2209-2220, 1993

A>Title: Epstein-Barr virus-induced genes: first lymphocyte-specific G protein-coupled

A/Reference number: A45680; MUID:93188173; PMID:8383238

A/Accession: B45680

A/Status: preliminary

A/Molecule type: nucleic acid

A/Residues: 1-361 <BIR>

A/Cross-references: GB:L08177; NID:g292056; PIDN:AAA35924.1; PID:g292057

A/Experimental source: B-lymphocytes

A/Note: sequence extracted from NCBI backbone (NCBIN:127096, NCBI:P:127097)

C/Superfamily: ATP receptor P2u

C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match

Best Local Similarity 21.3%; Score 379.5; DB 2; Length 361;

Matches 94; Conservative 84; Mismatches 152; Indels 31; Gaps 11;

QY 1 MQAVDNLT----SAPGNTSLCTRDYKITQVLPFLYTLVFLVGLITNGLAMRIFFQIRSK 56

DB 3 IQMANNFTPPSATPGNDCDLYAHSTARIWPLHYSLVFIIGLVGNLLALVWIVQNRKK 62

QY 57 SN-FIIFLNVTISDLMLITFPKIL-----SDAKLTGTRFVQCVTSVIFYFMYI 110

DB 63 INSTLYTNLVIDILFTLTALTRIAYANGFDWRIGDA-----LCRTALVFIINTYIA 117

QY 111 SISPLGLITIDRYOKTRPFTSNPKNLGAKILSVIWIWAFMFLSLPNNI--LTNRQPR 168

DB 118 GVNFTCLSIDRFIAVHPLAVNKKIRIEHAKGVCFWILVFAQTLLPLINPMSKQAE 177

QY 169 DKNVKCSFLKSEFGLVWHEIYNYCCQVIFWNLIVIVCYTLITKELYRS-----YVRT 223

DB 178 RITCMYEPNFBETKSLPW--ILLGACFGYVLPFIILICYSCCKLFRFAKQNPITEK 235

QY 224 RGVGKVPKKNVKNVFIIVAVFFICFPVFFHARIPYTLSTQTR--DVPDCTAENTLFFYK 281

DB 236 SGVKN--KALNT-IILIVVFLCTFPHVAILQHKMLKRLRFSNLECSQRHFSQISLH 291

QY 282 STLWLTSLNACLDPEIYFELCKSFNSLSMLKCPNSATSLSQDNRKKEQDGDGPNBETP 341

DB 292 FTVCLMNFNCMDPPIYFACKYKRVMLK-RQVSVSISAVKGAPEENSREMTETQ 350

QY 342 M 342



Db 351 M 351

RESULT 4

S63666

platelet activating factor receptor - mouse

C:Species: Mus musculus (house mouse)

C>Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 20-Jun-2000

C:Accession: S63666

R:Shih, S.; Matsuda, Y.; Nakamura, M.; Waga, I.; Kume, K.; Izumi, T.; Shimizu, T.

Biochem. J. 314, 671-678, 1996

A:Title: A murine platelet-activating factor receptor gene: cloning, chromosomal localization

A:Reference number: S63666; MUID:96233129; PMID:8670084

A:Accession: S63666

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-341 <ISH>

A:Cross-references: EMBL:D50872; NID:g1256924; PIDN:BAA09468.1; PID:g1256925

C:Superfamily: ATP receptor P2u

Query Match 20.6%; Score 366; DB 2; Length 341;

Best Local Similarity 29.9%; Pred. No. 4e-24;

Matches 96; Conservative 64; Mismatches 133; Indels 28; Gaps 10;

20 DYKIQVLPFLYTLVFFVGLITNGLAMRIFQI--RSKSNFI-IFLKNVTVIDLLMILT 76

10 DSEFRYLPFIYVSVIFILGVVANGYLVFANLYPSKLNKIKIFWNLTMADLLFLIT 69

77 PPKILSDAKLGTGLRTFVCQVTSVIFYPMYISIFLGLITIDRYOKTRPPTSNPK 136

70 LPLMIVVYNEGDWILFNLCNAGCLFFINTYCSVAFGLVITNRYQAVAYPIKTAQAT 129

137 NLLGAKILSVVIMAFM-----FLLSLPNMILTNRQPRDKNVKCC-----S 176

130 TRKRGISLILVSVIVATASYFLATSTNVLNPKDGSNITRCFEHYEPYSVILVHV 189

189 IVNYICQVIFWNLFI-VIVCYTLITKELYRSYVTRGVKVRKKNVVFIIIAVFFI 247

190 FIAFCFLVFLFIYCNLVIIHTLTPMRQQ--RKAGV---KRRALMWVCTVLAFFII 243

248 CFVPEFPIARIPTLSQTRDVPDCTAENTLFVYKESITLWLTSLNACLDPEIYFCLKSFRN 307

244 CFVPHVVLFWTLAEIG--YQNFHOAINDAHQITLCLSTNCVLDPEIYCFCLKFRK 301

308 -----SLISMLKCPNSATS 321

302 HLSEKFKYSMRSRKC-SRATS 321

RESULT 5

S43252

platelet-activating factor receptor - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 20-Oct-1994 #sequence\_revision 10-Nov-1995 #text\_change 24-Nov-1999

C:Accession: S43252

R:BiCo, H.; Honda, Z.; Nakamura, W.; Shimizu, T.

Eur. J. Biochem. 221, 211-218, 1994

A:Title: Cloning, expression and tissue distribution of rat platelet-activating-factor-

A:Reference number: S43252; MUID:94222063; PMID:8168510

A:Accession: S43252

A:Molecule type: mRNA

A:Residues: 1-341 <BIT>

A:Cross-references: GB:U04740; NID:g470384; PIDN:AAA18422.1; PID:g470385

C:Superfamily: ATP receptor P2u

Query Match 20.4%; Score 362; DB 2; Length 341;

Best Local Similarity 28.9%; Pred. No. 8.8e-24;

Matches 96; Conservative 66; Mismatches 120; Indels 50; Gaps 10;

20 DYKIQVLPFLYTLVFFVGLITNGLAMRIF--FQIRSKSNFIIFLKNVTVIDLLMILT 76

10 DSEFRYLPFIYVSVIFILGVVANGYLVFATLYPSKLNKIKIFWNLTVADLLFLMT 69

QY 77 PPKILSDAKLGTGLRTFVCQVTSVIFYPMYISIFLGLITIDRYOKTRPPTSNPK 136

Db 70 LPLMIVVYNEGDWILFNLCNAGCLFFINTYCSVAFGLVITNRYQAVAYPIKTAQAT 129

QY 137 NLLGAKILSVVIMAFM-----FLLSLPNMILTNRQPRDKNVKCC-----S 176

Db 130 TRKRGISLILVSVIVATASYFLATSTNVLNPKDGSNITRCFEHYEPYSVILVHV 189

QY 177 FKSEFGLVWHEIYNYICQVIFWNLFI-VIVCYTLITKELYRSYVTRGVKVRKKNV 236

Db 190 FITSCFFLVFF-----LIFYCNMVI--HTLLTRP-----VROQRKPEVKKRALMW 233

QY 237 KVFIILAVFFCFVPEFPIARIPTLSQTRDVPDCTAENTLFVYKESITLWLTSLNACLDPE 296

Db 234 -VCTVIAVFCVPHVVLFWTLAEIG--YQNFHOAINDAHQITLCLSTNCVLDPE 290

QY 297 IYFCLKSFRN-----SLISMLKCPNSATS 321

Db 291 IYCFCLKFRKHLSEKFKYSMRSRKC-SRATS 321

RESULT 6

I50241

G protein-coupled receptor GHI - chicken

N:Alternate names: purinoceptor GHI

C:Species: Gallus gallus (chicken)

C>Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 02-Jun-2000

C:Accession: I50241; JC4618

R:Kaplan, M.H.; Smith, D.I.; Sundick, R.S.

J. Immunol. 151, 628-636, 1993

A:Title: Identification of a G protein coupled receptor induced in activated T cells.

A:Reference number: I50241; MUID:93329058; PMID:8393036

A:Accession: I50241

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-308 <AP>

A:Cross-references: GB:L06109; NID:g304383; PIDN:AAB05587.1; PID:g304384

R:Webb, T.E.; Kaplan, M.G.; Barnard, E.A.

Biochem. Biophys. Res. Commun. 219, 105-110, 1996

A:Title: Identification of GHI as a P2Y purinoceptor: P2Y5.

A:Reference number: JC4618; MUID:96190677; PMID:8619790

A:Accession: JC4618

A:Molecule type: mRNA

A:Residues: 1-308 <WEB>

A:Cross-references: GB:L06109; NID:g304383; PIDN:AAB05587.1; PID:g304384

A:Experimental source: T-cells

C:Comment: This receptor plays a role in T-cell activation.

C:Genetics:

A:Gene: P2Y5

C:Superfamily: ATP receptor P2u

C:Keywords: G protein-coupled receptor; transmembrane protein

F15-40/Domain: transmembrane #status predicted <TM1>

F151-74/Domain: transmembrane #status predicted <TM2>

F189-109/Domain: transmembrane #status predicted <TM3>

F133-153/Domain: transmembrane #status predicted <TM4>

F177-201/Domain: transmembrane #status predicted <TM5>

F227-248/Domain: transmembrane #status predicted <TM6>

F269-292/Domain: transmembrane #status predicted <TM7>

Query Match 20.1%; Score 357.5; DB 2; Length 308;

Best Local Similarity 29.5%; Pred. No. 1.9e-23;

Matches 87; Conservative 68; Mismatches 125; Indels 15; Gaps 8;

14 TSLCTRDKYIKQVLPFLYTLVFFVGLITNGLAMRIF--FQIRSKSNFIIFLKNVTVIDLL 72

3 SSNCSTEDSFYKTLGYGVFVGLIANGCAVIFFTLKVNETTMMNLAIISDLL 62

73 MLTTPFKILSDAKLGTGLRTFVCQVTSVIFYPMYISIFLGLITIDRYOKTRPPT 132

63 FVFTLPFIYFV-VRNWPFPGDVLCKISVTLFYTNMYGSIILFLACISVDRLAIVHPFRS 121

133 SNPKNLLGAKILSVVIMAFMFLSLPNMILTNRQPRDKNVKCC--SFLKSEFGLVWHE 189

Db 122 KTLRKNARIVCVAVWITVLAGSTPASFFPOSTNRQ-NTEQRTCFENFPESTWKYLSR 180  
 QY 189 IVNYICQVIFWFLNVLIVCYTLTKELYSYVTRGVKPRKKNVVFIIIAVFFFC 248  
 Db 181 IVIETIEIVGFFIPLINVTCTMTWRLINKPLTLR--NKLKSKKVLKMFVHLVIFPCF 238  
 QY 249 FVPHFARIPYTLQTRDVFDC--TAENTLFYVKESTLMTSLNACLDPFIYFF 300  
 Db 239 FVPINITILYSLMRTQTWINCNVVAVRTVIFV---TLCIAVSNCCDFPIYIF 290

RESULT 7  
 S15403  
 angiotensin II receptor type 1 - bovine  
 C:Species: Bos primigenius indicus x Bos primigenius taurus (cattle)  
 C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 24-Nov-1999  
 R:Saeki, K.; Yamano, Y.; Bardhan, S.; Iwai, N.; Murray, J.J.; Hasegawa, M.; Matsuda, Y.  
 Nature 351, 230-233, 1991  
 A:Title: Cloning and expression of a complementary DNA encoding a bovine adrenal angiotensin II receptor type 1  
 A:Reference number: S15403; MUID:91251900; PMID:2041569  
 A:Accession: S15403  
 A:Status: Preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-359 <RES>  
 A:Cross-references: GB:X62294; NID:g43; PIDN:CAAA44182.1; PID:g44  
 C:Superfamily: vertebrate rhodopsin

Query Match 19.1%; Score 339; DB 2; Length 359;  
 Best Local Similarity 27.9%; Pred. No. 9e-22; Mismatches 143; Indels 40; Gaps 10;  
 Matches 95; Conservative 62;

QY 26 VLFPFLYTLVLFVGLITNGL-AMRIFFQIRSKSNFIIFLKNVTISDLMLITLTPFKILSD 84  
 Db 29 IMIETLYSIIFVVGIFGNSLVVIVFYFMKLTAVSVFLLNALADLCFLTLPLMAVYT 88  
 QY 85 AKLTGPTLTFVCOVTSVIFFTWYISIFLGLITIDRYOKTTPFKTSNPKLLGAKIL 144  
 Db 89 AMEYRWPFNGYLCKTASASVSNLYASVFLTCLSIDRYLAIVHPMKSRRLRTMLVAKVT 148  
 QY 145 SVVIAWAFVLLSLPNMILT-NRQPRDKNVKCSF-----LKSEFGLVWHEIVNYICQ 195  
 Db 149 CIIWLLAGLASLPPIIHRNVFFIENTNITVCAFYHESQNSTLPVGLGT-KNLTGLF-- 205  
 QY 196 VIFWFLNVLIVCYTLTKELYSYVTRGVKPRKKNVVFIIIAVFFICEVPHFA 255  
 Db 206 ----FPFLIILTSYTLWKLKAYEIQK--NKPRKDDIFKIILAIVLVFPF-----FS 252  
 QY 256 RIPYTLQTRDVF-----DCTAENTLFYVKESTLMTSLNACLDPFIYFFLCKSFNS 308  
 Db 253 WYPHQIFTFMDVLQGLIRCKIEDIVDTAMPITICLAYFNCLNPLFYGLGKFKKY 312  
 QY 309 LISMLK-CPNSATSLSQNRK-----KEQGGGDPNEETP 341  
 Db 313 FLQLLKYPAPKAKSHSLSTKMSTLSYRSPENGNSSTKKP 352

RESULT 8  
 T09508  
 intron 17 purinergic receptor P2Y5 - human  
 N:Alternate names: G-protein coupled receptor  
 C:Species: Homo sapiens (man)  
 C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 24-Nov-1999  
 R:Bohm, S.K.; Trumpp, A.; Khatin, L.M.; Kong, W.; Pavan, D.G.; Bunnett, N.W.  
 submitted to the EMBL Data Library, April 1997  
 A:Description: The human purinergic receptor P2Y5 is encoded in intron 17 of the retinoblastoma gene  
 A:Reference number: Z16705  
 A:Accession: T09508  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-344 <BOH>

A:Cross-references: EMBL:AF000546; NID:g2232068; PID:g2232069  
 C:Genetics:  
 A:Map position: 13  
 C:Superfamily: ATP receptor P2u  
 C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 19.0%; Score 338; DB 2; Length 344;  
 Best Local Similarity 26.4%; Pred. No. 1.1e-21; Mismatches 146; Indels 18; Gaps 8;  
 Matches 87; Conservative 79;

QY 13 NPSLCTRYKIKTQVLPFLYTLVLFVGLITNGLAMRIFF-QIRSKSNFIIFLKNVTISDL 71  
 Db 5 NSSHCFYNDSPKTYLYGCMFVGLVSNCAIYIFICVLKVRNETTTTMINLAWSDL 64  
 QY 72 LMILTFPEPKILSDAKLTGTPRTFTVCOVTSVIFFTWYISIFLGLITIDRYOKTTPFK 131  
 Db 65 LEVFTLPIRIFY-FTRRWPFGLDLCKISVLMFTNMYGSLFLTLCISVDRFLAIVVYFF 123  
 QY 132 TSNPKNLGAKILSVIWAFLSLPNMILTNRQPRDKNVK--SFLKSEFGLVWHE 188  
 Db 124 SKLTETKENAKIVCTGWLTVIGGSAPAVFVQSTHSQNNASEACFENPEATWKTLYLSR 183  
 QY 189 IVNYICQVIFWFLNVLIVCYTLTKELYSYVTRGVKPRKKNVVFIIIAVFFIC 248  
 Db 184 IVIETIEIVGFFIPLINVTCTMTWRLINKPLTLR--SKINTKVLKMFVHLIIFCFC 241  
 QY 249 FVPHFARIPYTLQTRDVFDC--TAENTLFYVKESTLMTSLNACLDPFIYFFLCKSF 305  
 Db 242 FVPYNINILYSLVTRQTFVNCVVAAVRTVYPI--TLCIAVSNCCDFPIYVYFTSDTI 298  
 QY 306 RNSLISMLKCPNSATSLSQNRKKEQGGD 335  
 Db 299 QNS-----IMKNQSVRR3-DFRFSEVHGAE 323

RESULT 9  
 I39418  
 angiotensin II receptor type 1b - human  
 C:Species: Homo sapiens (man)  
 C:Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 24-Nov-1999  
 R:Kuroda, S.  
 Biochem. Biophys. Res. Commun. 199, 467-474, 1994  
 A:Title: Novel subtype of human angiotensin II type 1 receptor: cDNA cloning and expression  
 A:Reference number: I39418; MUID:94183213; PMID:8135787  
 A:Accession: I39418  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-359 <RES>  
 A:Cross-references: GB:D13814; NID:g471120; PIDN:BAA02968.1; PID:g471121  
 C:Superfamily: vertebrate rhodopsin

Query Match 18.5%; Score 329; DB 2; Length 359;  
 Best Local Similarity 28.7%; Pred. No. 6.6e-21; Mismatches 137; Indels 34; Gaps 9;  
 Matches 92; Conservative 58;

QY 26 VLFPFLYTLVLFVGLITNGL-AMRIFFQIRSKSNFIIFLKNVTISDLMLITLTPFKILSD 84  
 Db 29 VMITLYSIIFVVGIFGNSLVVIVFYFMKLTAVSVFLLNALADLCFLTLPLMAVYT 88  
 QY 85 AKLTGPTLTFVCOVTSVIFFTWYISIFLGLITIDRYOKTTPFKTSNPKLLGAKIL 144  
 Db 89 AMEYRWPFNGYLCKTASASVSNLYASVFLTCLSIDRYLAIVHPMKSRRLRTMLVAKVT 148  
 QY 145 SVVIAWAFVLLSLPNMILT-NRQPRDKNVKCSF-----LKSEFGLVWHEIVNYICQ 195  
 Db 149 CIIWLLAGLASLPPIIHRNVFFIENTNITVCAFYHESQNSTLPGLGLTKNLSG--C- 205  
 QY 196 VIFWFLNVLIVCYTLTKELYSYVTRGVKPRKKNVVFIIIAVFFICEVPHFA 255  
 Db 206 ----FPFLIILTSYTLWKLKAYEIQK--NPNRNDIDIFRIIMAVLVPF-----FS 252  
 QY 256 RIPYTLQTRDVF-----DCTAENTLFYVKESTLMTSLNACLDPFIYFFLCKSFNS 308

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Db 253 WIPQITFTFDVLIIQGIIRDRIADIVDTAMPITIIWIAFNNCLNPLFYGLGKFKKD 312
QY 309 LISMLK-CPNSATSLSDNRK 328
Db 313 ILQLKVIIPPKAKSHSNLSTK 333

RESULT 10
34425
angiotensin II receptor type 1 - dog
C:Species: Canis lupus familiaris (dog)
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Nov-1999
C:Accession: S44425
R:Burns, L.; Clark, K.L.; Bradley, J.; Robertson, M.J.; Clark, A.J.L.
E:EBBS Lett. 343, 146-150, 1994
A:Title: Molecular cloning of the canine angiotensin II receptor. An AT1-like receptor
A:Reference number: S44425; MUID:94222186; PMID:8168620
A:Accession: S44425
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-359 <BUR>
A:Cross-references: PIDN:AA830674.1; PID:G546569
A:Experimental source: liver
A:Superfamily: vertebrate rhodopsin

Query Match 18.3%; Score 326; DB 2; Length 359;
Best Local Similarity 29.2%; Pred. No. 1.2e-20;
Matches 92; Conservative 54; Mismatches 147; Indels 22; Gaps 8;

QY 26 VLPFLLYTVLFFVGLIINGLA-MRIFQIRSKSNFIIFLKNVTVISDLMLITPPFKILSD 84
Db 29 VMIEPTLSIIIFVVGIFGNSLAVIIVFYFMKLTVASVFLNLALADLCFLTLPLWAVYT 88
QY 85 AKLGTGRLTFVCOVTSVIFVFTWYISISFLGLITIDRYOKTTRPKTSNPKNLGAKIL 144
Db 89 AMEYRWPFGNYLCKIASASVFNLYASVFLTCLSIDRYVAIVHPKSPVRMTLWAKVT 148
QY 145 SVVIWAFMFLSLPNNILTN-RQPRDNKVKCSF-----LKSEFGLVWHEIVNYICQ 195
Db 149 CIIWLLAGLASLPAIIHRNVFFIENTNITVCAPHYESQNSTLPIGLGLT-KNILGFL-- 205
QY 196 VIFWNLIVIVCVTLTKELYSYVTRGVGKVPKKNVKVFI-IIAVFFICFVPEFH 254
Db 206 ----FPFLIILTSYLLWKLKRAYEQK---NKPRNDIDFKIIMAVLFFFSWVPHQI 258
QY 255 ARIPYTLSTQTRDVEDCTAENTLFYVKESTLWLTSLNACLDPFIYFFLCKSFNLSMLK 314
Db 259 FTFLDVLIIQLGIHDCRIADIVDTAMPITICIAVFNNCLNPLFVGLGKFKKYFLQLLK 318
QY 315 -CPNSATSLSDNRK 328
Db 319 YIPPKAKSHSNLSTK 333

RESULT 11
148705
proteinase activated receptor 2 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Nov-1999
C:Accession: 148705
R:Nystedt, S.; Larsson, A.K.; Aberg, H.; Sundelin, J.
J. Biol. Chem. 270, 5950-5955, 1995
A:Title: The mouse proteinase-activated receptor-2 cDNA and gene. Molecular cloning and
A:Reference number: 148705; MUID:95197620; PMID:7890726
A:Accession: 148705
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-399 <RES>
A:Cross-references: EMBL:Z48043; NID:G663020; PIDN:CAA88097.1; PID:G663021
C:Superfamily: ATP receptor P2u

Query Match 18.3%; Score 325.5; DB 2; Length 399;
```

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Best Local Similarity 27.6%; Pred. No. 1.5e-20;
Matches 92; Conservative 73; Mismatches 141; Indels 27; Gaps 12;

QY 22 KITQVLFLYTVLFFVGLIINGLA-MRIFQIRSKSNFIIFLKNVTVISDLMLITPPFK 80
Db 74 KLTIVFLPVVVIIVFVGLPSGNALWIFLRTKKHPAVIYMANLALADLSVWPEFLK 133
QY 81 ILSDAKLGTPRLTFVCOVTSVIFVFTWYISISFLGLITIDRYOKTTRPKTSNPKNLG 140
Db 134 ISYHLGNWYVYGEALCKVLIGFYGNYCSILFMTCLSVQRYWVIVNPM--GHPKKAN 191
QY 141 AKI-LSVVIWAFMFLSLPNNIL--TNKQPRDNKVKCSFLKSEFGLVWHEIVNYICQV- 196
Db 192 IAVGSLALWLLIIFLVPIFYVMQTIYIPA-LNITTCVDVLPVLY-GDMFYFLSLA 249
QY 197 --IFWNLIVIVCVTLTKELYSYVTRGVGKVPKKNVKVFI-IIAVFFICFVPEFH 254
Db 250 IGVFLFPALLTASAYVLMIKLTRSSAMDEHSEKK--RQRAIRLIITVLAMFYCFAPSNL 307
QY 255 AR-IPYTLSTQTRDVEDCTAENTLFYVKESTLWLTSLNACLDPFIYFFLCKSFNLSML 313
Db 308 LLVHYFLIKTQ-----RQSHVVALYIVLALCLSTLNSCIDPFVYVYVSKDFRDHARNAL 361
QY 314 KCPNSAT-----SLSDNRKKEQDGDPEET 340
Db 362 LCRSVRTVNRMQISLS-SNKFSKSGSYSSST 393

RESULT 12
148857
angiotensin II receptor type 1 - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
C:Accession: A48857
R:Burns, K.D.; Inagami, T.; Harris, R.C.
Am. J. Physiol. 264, F645-F654, 1993
A:Title: Cloning of a rabbit kidney cortex AT1 angiotensin II receptor that is present
A:Reference number: A48857; MUID:93236091; PMID:7916579
A:Accession: A48857
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-359 <BUR>
A:Cross-references: GB:S59041; NID:G299614; PIDN:AA826239.1; PID:G299615
A:Experimental source: proximal tubule cells
A>Note: sequence extracted from NCBI Backbone (NCBIN:129600, NCBI:129601)
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 18.3%; Score 325; DB 2; Length 359;
Best Local Similarity 29.2%; Pred. No. 1.5e-20;
Matches 92; Conservative 55; Mismatches 146; Indels 22; Gaps 8;

QY 26 VLPFLLYTVLFFVGLIINGLA-MRIFQIRSKSNFIIFLKNVTVISDLMLITPPFKILSD 84
Db 29 VMIEPTLSIIIFVVGIFGNSLAVIIVFYFMKLTVASVFLNLALADLCFLTLPLWAVYT 88
QY 85 AKLGTGRLTFVCOVTSVIFVFTWYISISFLGLITIDRYOKTTRPKTSNPKNLGAKIL 144
Db 89 AMEYRWPFGNYLCKIASASVFNLYASVFLTCLSIDRYVAIVHPKSRRLRMTLWAKVT 148
QY 145 SVVIWAFMFLSLPNNILTN-RQPRDNKVKCSF-----LKSEFGLVWHEIVNYICQ 195
Db 149 CIIWLLAGLASLPAIIHRNVFFIENTNITVCAPHYESQNSTLPIGLGLT-KNILGFL-- 205
QY 196 VIFWNLIVIVCVTLTKELYSYVTRGVGKVPKKNVKVFI-IIAVFFICFVPEFH 254
Db 206 ----FPFLIILTSYLLWKLKRAYEQK---NKPRNDIDFKIIMAVLFFFSWVPHQI 258
QY 255 ARIPYTLSTQTRDVEDCTAENTLFYVKESTLWLTSLNACLDPFIYFFLCKSFNLSMLK 314
Db 259 FTFLDVLIIQLGIHDCRIADIVDTAMPITICIAVFNNCLNPLFVGLGKFKKYFLQLLK 318
QY 315 -CPNSATSLSDNRK 328
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Search completed: February 4, 2004, 14:30:59  
Job time : 21 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 4, 2004, 14:23:36 ; Search time 17 Seconds  
(without alignments)  
946.067 Million cell updates/sec

Title: US-09-780-576-2

Perfect score: 1778

Sequence: 1 MQAVDNLTSPAGNYSICTRD.....SQDNRRKKEODGDPNEETPM 342

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1778	100.0	342	1 P2YC HUMAN	Q9h244 homo sapien
2	1748	98.3	342	1 P2YC MACACA	Q95kc3 macaca fasc
3	1555.5	87.5	347	1 P2YC MOUSE	Q9cpv9 mus musculus
4	1528.5	86.0	343	1 P2YC RAT	Q9epx4 rattus norv
5	772	43.4	338	1 P2YX HUMAN	Q15391 homo sapien
6	741.5	41.7	338	1 P2YX MOUSE	Q9esg6 mus musculus
7	694	39.0	305	1 P2YX RAT	Q35881 rattus norv
8	488	27.4	319	1 H963 HUMAN	Q14626 homo sapien
9	411.5	23.1	375	1 GP34 MOUSE	Q9rlk6 mus musculus
10	409.5	23.0	381	1 GP34 HUMAN	Q9ucp5 homo sapien
11	394	22.2	342	1 PAFR HUMAN	P25105 homo sapien
12	382.5	22.1	342	1 PAFR CAVPO	P21556 cavia porce
13	379.5	21.3	361	1 EB12 HUMAN	P32249 homo sapien
14	367	20.6	345	1 CLT2 FIG	Q95n03 sus scrofa
15	366	20.6	341	1 PAFR RAT	Q62035 mus musculus
16	362	20.4	341	1 PAFR RAT	P46002 rattus norv
17	357.5	20.1	308	1 P2Y5 CHICK	P32250 gallus gall
18	347.5	19.5	345	1 CLT2 HUMAN	Q9ns75 homo sapien
19	347.5	19.5	537	1 P2Y8 XENLA	P79928 xenopus lae
20	344	19.3	309	1 CLT2 MOUSE	Q928a1 mus musculus
21	339.5	19.1	309	1 CLT2 RAT	Q924t9 rattus norv
22	339	19.1	359	1 AG2R BOVIN	P25104 bos taurus
23	338	19.0	344	1 P2Y5 HUMAN	P43657 homo sapien
24	334	18.8	359	1 AG2R SHEEP	O77590 ovis aries
25	334	18.8	367	1 GP17 HUMAN	Q13304 homo sapien
26	329	18.5	359	1 AG2S HUMAN	Q13725 homo sapien
27	328	18.4	340	1 CLT1 FIG	Q35n02 sus scrofa
28	327	18.4	359	1 AG2R FIG	P43240 canis fami
29	326	18.3	359	1 AG2R CANFA	P55086 mus musculus
30	325.5	18.3	399	1 PAR2 MOUSE	P34976 oryctolagus
31	325	18.3	359	1 AG2R RABIT	P30556 homo sapien
32	321	18.1	359	1 AG2R HUMAN	Q9wv26 cavia porce
33	320	18.0	359	1 AG2R_CAVPO	

#### ALIGNMENTS

##### RESULT 1

ID	P2YC HUMAN	STANDARD;	PRT;	342 AA.
AC	Q9H244;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	P2Y purinoceptor 12 (P2Y12) (P2Y12 platelet ADP receptor) (P2Y(ADP))			
DE	(ADP-glucose receptor) (ADPG-R) (P2Y(AC)) (P2Y(cyc)) (P2T(AC))			
DE	(SPI999)			
GN	P2RY12 OR HORK3			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21037966; PubMed=11196645;			
RA	Hollopeter G., Jantzen H.-M., Vincent D., Li G., England L.,			
RA	Ramakrishnan V., Yang R.-B., Nurdan P., Nurdan A., Julius D.J.,			
RA	Conley P.B.;			
RT	Identification of the platelet ADP receptor targeted by			
RT	antithrombotic drugs.;			
RL	Nature 409:202-207(2001).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Hyothalamus;			
RX	MEDLINE=21269433; PubMed=11104774;			
RA	Zhang F.L., Luo L., Gustafson E., Lachowicz J., Smith M., Qiao X.,			
RA	Liu Y.-H., Chen G., Pramanik B., Laz T.M., Palmer K., Bayne M.,			
RA	Monsma F.J. Jr.;			
RT	"ADP is the cognate ligand for the orphan G protein-coupled receptor			
RT	SP1999.;"			
RL	J. Biol. Chem. 276:8608-8615(2001).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RX	MEDLINE=21394281; PubMed=11502873;			
RA	Takasaki J., Kamchaya M., Saito T., Matsumoto M., Matsumoto S.-I.,			
RA	Ohishi T., Soga T., Matsushima H., Furuichi K.;			
RT	"Molecular cloning of the platelet P2T(AC) ADP receptor:			
RT	pharmacological comparison with another ADP receptor, the P2Y1			
RT	receptor.;"			
RL	Mol. Pharmacol. 60:432-439(2001).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RA	Reinscheid R.K., Nockhacker H.-P., Wang Z., Zeng J., Ehlerl P.J.,			
RA	Civelli O.;			
RT	"ADP-glucose activates a G-protein coupled receptor and inhibits			
RT	smooth muscle contractions.;"			
RL	Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RA	Takeda S., Kadowaki S., Haga T., Takaesu H., Mitaku S.;			
RT	"Identification of G protein-coupled receptor genes from the human			
RT	genome sequence.;"			

34	320	18.0	370	1 P2Y9 HUMAN	Q99677 homo sapien
35	319.5	18.0	365	1 GP68 HUMAN	Q15743 homo sapien
36	319	17.9	359	1 AG2R RAT	P25095 rattus norv
37	319	17.9	359	1 AG2S RAT	P29089 rattus norv
38	318	17.9	359	1 AG2R MOUSE	P29754 mus musculus
39	318	17.9	361	1 P2Y4 MOUSE	Q9j187 mus musculus
40	316.5	17.8	398	1 OPRM RAT	P33535 rattus norv
41	316	17.8	359	1 AG2S MOUSE	P29755 mus musculus
42	316	17.8	377	1 APJ RAT	Q9jhg3 rattus norv
43	316	17.8	397	1 PAR2 RAT	Q63645 rattus norv
44	313.5	17.6	380	1 APJ HUMAN	P35414 homo sapien
45	313.5	17.6	401	1 OPRM FIG	Q95247 sus scrofa

Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

```

RL  SEQUENCE FROM N.A.
RN  MEDLINE=22388257; PubMed=12477932;
RC  TISSUE=Prostate;
RX  Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA  Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA  Altschul S.F., Zdobych B., Bustow K.H., Schaefer C.F., Bhat N.K.,
RA  Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA  Datchenko M., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA  Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA  Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA  Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA  Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA  Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA  Villalon D.K., Muzny D.N., Sodergren E.J., Lu X., Gibbs R.A.,
RA  Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA  Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA  Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA  Rodriguez A.C., Grinnwood J., Schmutz J., Myers R.M.,
RA  Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,
RA  Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT  "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences."
RL  Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
CC  -!- FUNCTION: Receptor for ADP and ATP coupled to G-proteins that
inhibit the adenylyl cyclase second messenger system. Not
activated by UDP and UTP. Involved in platelets aggregation.
CC  -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC  -!- TISSUE SPECIFICITY: Highly expressed in the platelets, lower
levels in the brain. Lowest levels in the lung, appendix,
pituitary and adrenal gland. Expressed in the spinal cord and in
the fetal brain.
CC  -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC  -----
DR  EMBL; AF313449; AAG48944.1; -
DR  EMBL; AF321815; AAK00948.1; -
DR  EMBL; AB052684; BAK60824.1; -
DR  EMBL; AF310685; AAL32292.1; -
DR  EMBL; AB083596; BAB89309.1; -
DR  EMBL; BC017898; BAH17898.1; -
DR  Genew; HGNC:18124; P2RY12.
DR  MIM; 600515; -
DR  GO; GO:0007599; P:hemostasis; NAS.
DR  InterPro; IPR000276; GPCR_Rhodopsn.
DR  InterPro; IPR005394; P2Y12_putnrcptor.
DR  Pfam; PF00001; 7tm1; 1.
DR  PRINTS; PR00237; GPCR_Rhodopsn.
DR  PRINTS; PR01569; P2Y12_P2RY12.
DR  PROSITE; PS00237; G-PROTEIN RECEPTOR F1_1; FALSE_NEG.
DR  PROSITE; PS00262; G-PROTEIN RECEPTOR F1_2; 1.
KW  G-protein coupled receptor; Transmembrane; Glycoprotein.
FT  DOMAIN 1 25 EXTRACELLULAR (POTENTIAL).
FT  TRANSMEM 26 46 1 (POTENTIAL).
FT  DOMAIN 47 58 CYTOPLASMIC (POTENTIAL).
FT  TRANSMEM 59 79 2 (POTENTIAL).
FT  DOMAIN 80 99 EXTRACELLULAR (POTENTIAL).
FT  TRANSMEM 100 120 3 (POTENTIAL).
FT  DOMAIN 121 142 CYTOPLASMIC (POTENTIAL).
FT  TRANSMEM 143 163 4 (POTENTIAL).
FT  DOMAIN 164 191 EXTRACELLULAR (POTENTIAL).
FT  TRANSMEM 192 212 5 (POTENTIAL).
FT  DOMAIN 213 233 CYTOPLASMIC (POTENTIAL).
FT  TRANSMEM 234 254 6 (POTENTIAL).
FT  DOMAIN 255 281 EXTRACELLULAR (POTENTIAL).
FT  -----
FT  TRANSMEM 282 302 7 (POTENTIAL).
FT  DOMAIN 303 342 CYTOPLASMIC (POTENTIAL).
FT  BY SIMILARITY.
FT  CARBOHYD 97 175 N-LINKED (GLCNAC...) (POTENTIAL).
FT  CARBOHYD 13 13 N-LINKED (GLCNAC...) (POTENTIAL).
SQ  SEQUENCE 342 AA; 39438 MW; 8553D2746C89176D CRC64;
Query Match 100.0%; Score 1778; DB 1; Length 342;
Best Local Similarity 100.0%; Pred. No. 3.7e-117;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQAVDNLSAPGNTSLCTRDYKTIQVLPFLIYTVLFFVGLITNGLAMRIFPQIRSKNFI 60
DB 1 MQAVDNLSAPGNTSLCTRDYKTIQVLPFLIYTVLFFVGLITNGLAMRIFPQIRSKNFI 60
QY 61 IFKNTVSDLLMLTLPFPKILSDAKLTGRLTFCVQTSVIFFTMYISIFLGLITI 120
DB 61 IFKNTVSDLLMLTLPFPKILSDAKLTGRLTFCVQTSVIFFTMYISIFLGLITI 120
QY 121 DRYQKTRFPKTSNPKNLGAKILSVIWAFLSLNPMILTNRPQDKNKKCSFLKS 180
DB 121 DRYQKTRFPKTSNPKNLGAKILSVIWAFLSLNPMILTNRPQDKNKKCSFLKS 180
QY 181 EFGVLVHEIVNYICQVIFWNLIVIVCYTITLITKELYSYVTRGVGKPKVNVKVI 240
DB 181 EFGVLVHEIVNYICQVIFWNLIVIVCYTITLITKELYSYVTRGVGKPKVNVKVI 240
QY 241 IIAVFFICFVPHFARIPTYSQTRDVEDCTAENTLFYVKESTLWLTSLNACLPFIYFF 300
DB 241 IIAVFFICFVPHFARIPTYSQTRDVEDCTAENTLFYVKESTLWLTSLNACLPFIYFF 300
QY 301 LCKSFNLSMLKCPNSATLSQDNRRKKEQGGDPNEETPM 342
DB 301 LCKSFNLSMLKCPNSATLSQDNRRKKEQGGDPNEETPM 342
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RESULT 2
P2YC_MACFA STANDARD; PRT; 342 AA.
ID P2YC_MACFA
AC Q95KC3; Q95GT8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE P2Y purinoceptor 12 (P2Y12).
GN P2RY12.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Frontal cortex, and Medulla oblongata;
RA Oeada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA Suzuki Y., Sugano S., Hashimoto K.;
RT "Isolation of full-length cDNA clones from macaque brain cDNA
libraries."
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor for ADP and ATP coupled to G-proteins that
inhibit the adenylyl cyclase second messenger system (By
similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; AB056385; BAB33041.1; -

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DR EMBL; AB062981; BAB60747.1; -.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PRINTS; PR01569; P2Y12_PRRNCPTR.
DR PROSITE; PS00237; G-PROTEIN RECP_F1_1; FALSE NEG.
DR PROSITE; PS00262; G-PROTEIN RECP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 25 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 26 46 1 (CYTOPLASMIC (POTENTIAL)).
FT DOMAIN 47 58 2 (CYTOPLASMIC (POTENTIAL)).
FT TRANSMEM 59 79 3 (POTENTIAL).
FT DOMAIN 100 120 4 (CYTOPLASMIC (POTENTIAL)).
FT TRANSMEM 121 142 5 (POTENTIAL).
FT DOMAIN 143 163 6 (CYTOPLASMIC (POTENTIAL)).
FT TRANSMEM 164 191 7 (POTENTIAL).
FT DOMAIN 192 212 8 (CYTOPLASMIC (POTENTIAL)).
FT TRANSMEM 213 233 9 (POTENTIAL).
FT DOMAIN 234 254 10 (CYTOPLASMIC (POTENTIAL)).
FT TRANSMEM 255 281 11 (POTENTIAL).
FT DOMAIN 282 302 12 (CYTOPLASMIC (POTENTIAL)).
FT TRANSMEM 303 342 13 BY SIMILARITY.
FT DISULFID 97 175 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 6 6 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 49 49 I -> T (IN REF. 1; BAB33041).
FT CONFLICT 89 89 A -> T (IN REF. 1; BAB33041).
SQ SEQUENCE 342 AA; 39479 MW; E93FC26BFF5EC4C CRC64;

Query Match 98.3%; Score 1748; DB 1; Length 342;
Best Local Similarity 98.0%; Pred. No. 4.5e-115;
Matches 335; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Cy 1 MQAVDNTSAPGNTSLCTRDYKTKITQVLFPILLYTVLFPVGLITNGLNLRFFQIRSKNFI 60
Db 1 MQAIDNLTSPAGNTSLCTRDYKTKITQVLFPILLYTVLFPVGLITNGLNLRFFQIRSKNFI 60
Qy 61 IFLKNTVISDLMLTTPFKILSDAKLGTGTPRTFCQVTSVIFVTMTWISIFLGLITI 120
Db 61 IFLKNTVISDLMLTTPFKILSDAKLGTGTPRTFCQVTSVIFVTMTWISIFLGLITI 120
Qy 121 DRYQKTRPFTKSNPKNLGAKILSVVINAFLSLPMLNLTNRPRDNKVKKCSFLKS 180
Db 121 DRYQKTRPFTKSNPKNLGAKILSVLINAFLSLPMLNLTNRPRDNKVKKCSFLKS 180
Qy 181 EFGVLWHEIYNYICQVFWINFLIVICVTLITKELYRSYVTRTGKVPKKNVKKVFI 240
Db 181 EFGVLWHEIYNYICQVFWINFLIVICVTLITKELYRSYVTRTGKVPKKNVKKVFI 240
Qy 241 IIAVFFICFPFFHAPRIPYTLSTQTRDVFDCATNTLFFVKESTLWTLNACLDPPIYFF 300
Db 241 IIAVFFICFPFFHAPRIPYTLSTQTRDVFDCATNTLFFVKESTLWTLNACLDPPIYFF 300
Qy 301 LCKSFRNSLSMLKCPNSATLSQDNKKEQDGDGDPNEETPM 342
Db 301 LCKSFRNSLSMLKCPNSATLSQDNKKEQDGDGDPNEETPM 342

RESULT 3
P2YC_MOUSE
ID P2YC_MOUSE STANDARD; PRT; 347 AA.
AC Q9CFV9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE P2Y purinoceptor 12 (P2Y12).
GN P2Y12
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OC NCBI_TaxID=10090;

```

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RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Hippocampus, and Testis;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamahaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schram L.M., Stauber F., Suzuki R., Tomita M., Wagner T., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boifelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang X.H., Weitz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kontsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN SEQUENCE FROM N.A.
RX MEDLINE=22389257; PubMed=12477932;
RA Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Wozney K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield J.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:15899-15903(2002).
CC -!- FUNCTION: Receptor for ADP and ATP coupled to G-proteins that
CC inhibit the adenyl cyclase second messenger system (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC
CC EMBL; AK013804; BAB29000.1;
CC EMBL; AK014807; BAB29561.1;
CC EMBL; BC025428; AAB25428.1;
CC EMBL; BC027381; AAB27381.1;
CC MGD; MGI:1918089; P2Y12.
CC GO; GO:0005887; C:integral to plasma membrane; IC.
CC GO; GO:0001609; F:adenosine receptor, G-protein coupled activity; IMP.
CC GO; GO:0001621; F:platelet ADP receptor activity; IMP.
CC GO; GO:0007188; P:G-protein signaling, coupled to cAMP nucleo. .; IMP.
CC GO; GO:0030188; P:platelet activation; IMP.
CC InterPro; IPR000276; GPCR_Rhodopsn.
CC InterPro; IPR005394; P2Y12_purinocptor.

```

```

DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PRINTS; PR01569; P2Y12PRNCPT.
DR PROSITE; PS00237; G-PROTEIN RECP F1_1; FALSE_NEG.
DR PROSITE; PS00262; G-PROTEIN RECP F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 31
FT TRANSMEM 32 52
FT DOMAIN 53 64
FT TRANSMEM 65 85
FT DOMAIN 86 105
FT TRANSMEM 106 126
FT DOMAIN 127 148
FT TRANSMEM 149 169
FT DOMAIN 170 197
FT TRANSMEM 198 218
FT DOMAIN 219 239
FT TRANSMEM 240 260
FT DOMAIN 261 287
FT TRANSMEM 288 308
FT DOMAIN 309 347
FT TRANSMEM 348 374
FT DISULFID 103 181
FT CARBOHYD 7 7
FT CARBOHYD 12 12
FT CONFLICT 3
SQ SEQUENCE 347 AA; 39473 MW; F107488E57E025F1 CRC64;

Query Match
Best Local Similarity 87.5%; Score 1555.5; DB 1; Length 347;
Matches 299; Conservative 16; Mismatches 21; Indels 1; Gaps 1;

QY 6 NLTSAPGNISLCTRDYKIQVLFLLYVLPFFVGLITNGLAMRIFFQIRKSNFIIFLKN 65
DB 12 NTSIPGSLTCDYKIQVLFLLYVLPFFVGLITNGLAMRIFFQIRKSNFIIFLKN 71
QY 66 TVISDLMLFPFKILSDAKLGTGPLRTFVQVTSVIFFTWYISIFGLITIDRYOK 125
DB 72 TVISDLMLFPFKILSDAKLGTGPLRTFVQVTSVIFFTWYISIFGLITIDRYOK 131
QY 126 TTRPFTSNPNKLLGAKILSVIWAFFLLSLPNMILTNRQPRDKNVKCSFLKSEFGLV 185
DB 132 TTRPFTSNPNKLLGAKILSVIWAFFLLSLPNMILTNRQPRDKNVKCSFLKSEFGLV 191
QY 186 WHEIYNYICQVIFNFIIVLCVTLTKELYRSYVTRGVKPRKKNVKKVFIIVAVF 245
DB 192 WHEIYNYICQVIFNFIIVLCVTLTKELYRSYVTRGVKPRKKNVKKVFIIVAVF 251
QY 246 FICFVPPHFAIPYTLSTQTRVDFDCTAENTLFYVKESTLWLTSLNACLDPPFIYFLCKSF 305
DB 252 FICFVPPHFAIPYTLSTQTRVDFDCTAENTLFYVKESTLWLTSLNACLDPPFIYFLCKSF 311

RESULT 4
P2YC_RAT ID P2YC_RAT STANDARD; PRT; 343 AA.
AC Q9EPX4;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE P2Y purinoceptor 12 (P2Y12) (P2Y12 platelet ADP receptor).
GN P2Y12.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Cranial; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=21037966; PubMed=11196645;

```

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RA Holloper G., Jantzen H.-M., Vincent D., Li G., England L.,
RA Ramakrishnan V., Yang R.-B., Nurdan P., Nurdan A., Julius D.J.,
RA Conley P.B.;
RT "Identification of the platelet ADP receptor targeted by
RT antithrombotic drugs.";
RL Nature 409:202-207(2001).
CC -!- FUNCTION: Receptor for ADP and ATP coupled to G-proteins that
CC inhibit the adenylyl cyclase second messenger system (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF313450; AAC48945.1;
DR InterPro; IPR00276; GPCR_Rhodopsn.
DR InterPro; IPR005394; P2Y12_purinocptor.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PRINTS; PR01569; P2Y12PRNCPT.
DR PROSITE; PS00237; G-PROTEIN RECP F1_1; FALSE_NEG.
DR PROSITE; PS00262; G-PROTEIN RECP F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 31
FT TRANSMEM 32 52
FT DOMAIN 53 64
FT TRANSMEM 65 85
FT DOMAIN 86 105
FT TRANSMEM 106 126
FT DOMAIN 127 148
FT TRANSMEM 149 169
FT DOMAIN 170 197
FT TRANSMEM 198 218
FT DOMAIN 219 239
FT TRANSMEM 240 260
FT DOMAIN 261 287
FT TRANSMEM 288 308
FT DOMAIN 309 343
FT DISULFID 103 181
FT CARBOHYD 7 7
FT CARBOHYD 12 12
FT SEQUENCE 343 AA; 39047 MW; 7AEOAFCE6674136 CRC64;

Query Match
Best Local Similarity 86.0%; Score 1528.5; DB 1; Length 343;
Matches 293; Conservative 17; Mismatches 22; Indels 5; Gaps 1;

QY 6 NLTSAPGNISLCTRDYKIQVLFLLYVLPFFVGLITNGLAMRIFFQIRKSNFIIFLKN 65
DB 12 NTSIPGSLTCDYKIQVLFLLYVLPFFVGLITNGLAMRIFFQIRKSNFIIFLKN 71
QY 66 TVISDLMLFPFKILSDAKLGTGPLRTFVQVTSVIFFTWYISIFGLITIDRYOK 125
DB 72 TVISDLMLFPFKILSDAKLGTGPLRTFVQVTSVIFFTWYISIFGLITIDRYOK 131
QY 126 TTRPFTSNPNKLLGAKILSVIWAFFLLSLPNMILTNRQPRDKNVKCSFLKSEFGLV 185
DB 132 TTRPFTSNPNKLLGAKILSVIWAFFLLSLPNMILTNRQPRDKNVKCSFLKSEFGLV 191
QY 186 WHEIYNYICQVIFNFIIVLCVTLTKELYRSYVTRGVKPRKKNVKKVFIIVAVF 245
DB 192 WHEIYNYICQVIFNFIIVLCVTLTKELYRSYVTRGVKPRKKNVKKVFIIVAVF 251
QY 246 FICFVPPHFAIPYTLSTQTRVDFDCTAENTLFYVKESTLWLTSLNACLDPPFIYFLCKSF 305
DB 252 FICFVPPHFAIPYTLSTQTRVDFDCTAENTLFYVKESTLWLTSLNACLDPPFIYFLCKSF 311

```

306 RNSLISMLKCPNSATSLSQNRKKKGQGGDPNSETPM 343  
312 RNSLISMLRC-----STSGANKKKQGGDPSETPM 343

RESULT 5  
P2YX\_HUMAN  
IID P2YX\_HUMAN STANDARD; PRT; 338 AA.  
AC Q15391;  
15-JUL-1998 (Rel. 36, Created)  
15-JUL-1998 (Rel. 36, Last sequence update)  
28-FEB-2003 (Rel. 41, Last annotation update)  
UDP-glucose receptor (G protein-coupled receptor GPR105 OR KIAA0001).  
OS Homo sapiens (Human).  
OC Eukaryota; Euteozoa; Chordata; Craniata; Vertebrata  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea  
OC NCBI\_TaxId=9606;  
OX [1]  
[1] SEQUENCE FROM N.A.  
RC TISSUE=Bone marrow;  
RP MEDLINE=9605387; PubMed=7584026;  
RX Nomura N., Miyajima N., Suzuki T., Tanaka A., Kawata  
RA Sato S., Nagase T., Seki N., Ishikawa K.-I., Tabata  
RA "Prediction of the coding sequences of unidentified  
RT The coding sequences of 40 new genes (KIAA0001-KIAA  
RT analysis of randomly sampled cDNA clones from human  
RT cell line KG-1".  
RT DNA Res. 1:27-35(1994).  
RL [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21426338; PubMed=11524702;  
RA Joensuu T., Haemaelaeninen R., Yuan B., Johnson C.,  
RA Gasparini P., Zeilante L., Pirvola U., Pakarinen L.,  
RA de la Chapelle A., Sankila E.-M.;  
RT "Mutations in a novel gene with transmembrane domain  
RT syndrome type 3".  
RT Am. J. Hum. Genet. 59:673-684(2001).  
RL [3]  
RP FUNCTION.  
RX MEDLINE=20219108; PubMed=10753868;  
RA Chambers J.K., MacDonald L.E., Sarau H.M., Ames R.A.  
RA Foley J.J., Zhu Y., McLaughlin M.M., Murdock P., M  
RA Trill J., Swift A., Aiyar N., Taylor P., Vawter L.  
RA Szekeres P., Hervieu G., Scott C., Watson J.M., Mu  
RA Klein C., Bergsma D.J., Wilson S., Livi G.P.;  
RT "A G protein-coupled receptor for UDP-glucose.";  
RT J. Biol. Chem. 275:10767-10771(2000).  
RL [4]  
CC -!- FUNCTION: Receptor for UDP-glucose and other U  
CC G-proteins. Not activated by ATP, ADP, UTP o  
CC -!- SUBCELLULAR LOCATION: Integral membrane protei  
CC -!- TISSUE SPECIFICITY: Highest expression in the  
CC tissue, stomach and intestine, intermediate le  
CC spleen, lung and heart. Lowest levels in the k  
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN C  
CC  
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CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).

EMBL; D13662; BAA02791.1; -;  
DR EMBL; AF456925; AAL47764.1; -;  
DR GenBank; HGNC:16442; GPR105.  
DR GO; GO:0016021; C:intracellular membrane;  
DR GO; GO:0045029; P:UDP-activated nucleotide receptor  
DR GO; GO:0007186; P:G-protein coupled receptor prote  
DR InterPro; IPR000276; GPCR\_Rhodopsin.  
DR InterPro; IPR005466; UDPG\_Receptor.  
DR Pfam; PF00001; 7tm\_1; 1.

[illegible]

CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
CC  
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CC  
CC -----  
CC EMBL: D13626; BAA02791.1; --  
CC EMBL: AF456925; AAL47764.1; --  
CC Genew: HGNC:16442; GPR105.  
CC GO: GO:0016021; C:integral to membrane; NAS.  
CC GO: GO:0045029; F:UDP-activated nucleotide receptor activity; NAS.  
CC GO: GO:0007186; P:G-protein coupled receptor protein signalin...; NAS.  
CC InterPro: IPR000276; GPCR Rhodopsin.  
CC InterPro: IPR005466; UDPG receptor.  
CC Pfam: PFC0001; 7tm 1; 1.  
CC



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QY 64 KNTVISDLMLTPPKILSDAKLGTGLRTFVCQVTSVLFYFTMYISISFLGLITIDRY 123
DB 61 KNIVVAFLMGLTEPPKVLSDSGLPQLNVFVRSAVIFYNNVSVISAFGLISFDY 120
QY 124 QKTRPRTSPKPKLLGAKILSVVWAFMFLSLPNNMLTNRPDRDNKVKKCSFLKSEFG 183
DB 121 YKIVKPLVSVQSVNYSKVLVWVLMVLLAVENIILTNQSVKDVNTQCMELKNELG 180
QY 184 LWHEIVNYICQVFWNLFIIVCYTLTKELVRSVVRTRGVKPKVKNVVKVILIA 243
DB 181 RKWKASNYFVSFWVFLVLLTVFWVWITRKFKSHLKRKNSISVKRKSRIISVL 240
QY 244 VFFICVFPFHARIPYTLISQTRDVFDCDAENTLFFVKESTLWLTSLNACLDP 295
DB 241 AFVACFAPYHVARIPYTKSQTEGYSQAKETLLYTKETLLLSAANVCLDP 292

RESULT 8
H963_HUMAN
ID H963_HUMAN STANDARD; PRT; 319 AA.
AC O14626;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Probable G protein-coupled receptor H963.
GN H963.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Peripheral blood monocytes;
RC MEDLINE=9603606; PubMed=9370294;
RA Jacobs K.A., Collins-Racie L.A., Colbert M., Duckett M.,
RA Golden-Fleet M., Kelleher K., Kriz R., LaVallie E.R., Merberg D.,
RA Spaulding V., Stover J., Williamson M.J., McCoy J.M.;
RT "A genetic selection for isolating cDNAs encoding secreted proteins.";
RL Gene 198:289-296(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21426338; PubMed=11524702;
RA Joensuu T., Haemelaenen R., Yuan B., Johnson C., Tegelsberg S.,
RA Gasparini P., Zelante L., Pirvola U., Pakarinen L., Lehesjoki A.-E.,
RA de la Chapelle A., Sankila E.-M.;
RT "Mutations in a novel gene with transmembrane domains underlie Usher
RT syndrome type 3.";
RL Am. J. Hum. Genet. 69:673-684 (2001).
CC -!- FUNCTION: ORPHAN RECEPTOR.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL; AF002986; AAC51846.1; -
DR EMBL; AF411849; AAL47763.1; -
DR GO; GO:0016021; C: integral to membrane; NAS.
DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. .; NAS.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHDOPSN
DR PROSITE; PS00237; G-PROTEIN RECP_F1_1; 1.
DR PROSITE; PS00262; G-PROTEIN RECP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 21 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 22 42 1 (POTENTIAL).
```

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FT DOMAIN 43 48
FT TRANSMEM 49 69
FT DOMAIN 70 89
FT TRANSMEM 90 110
FT DOMAIN 111 132
FT TRANSMEM 133 153
FT DOMAIN 154 181
FT TRANSMEM 182 202
FT DOMAIN 203 224
FT TRANSMEM 225 245
FT DOMAIN 246 268
FT TRANSMEM 269 289
FT DOMAIN 290 319
FT CARBOHYD 3
SQ SEQUENCE 319 AA; 36754 MW; 7989821C10841114 CRC64;

Query Match 27.4%; Score 488; DB 1; Length 319;
Best Local Similarity 34.5%; Pred. No. 2.2e-27;
Matches 112; Conservative 62; Mismatches 125; Indels 26; Gaps 9;

QY 13 NTSCLTRDYKITQVLPPLLYTVLFFVGLITNGLAMRIFQIRSKSNFI-IFLKNTVISDL 71
DB 3 NSSFFCPVYKDEP-FTVFFYLVFLVGIIGSCFATWAFIQKNTNHRVCVSIYLLNLTADF 61
QY 72 LMILTFPEKILSDAKLGTGP--LRTEVCQVTSVLFYFTMYISISFLGLITIDRYQKTRP 129
DB 62 LUTLALPKIVVD--LGAPWKLKIFHCQVACLIYNNMLSIIFLAFVSDIRCLQLTHS 119
QY 130 FKTSNPKLLGAKILSVVWAFMFLSLPNNMLTNRPDRDNKVKKCSFLKSEFGLVWHEI 189
DB 120 CKIVRIQEPGFAMISTVWMLVLLIMVNNMIPKIDKEKSNVCGMEFKKEFGKRNWELL 179
QY 190 VNYICQVFWINP-LIVIVCVTLTKELYSVYVTRGVKVPK-KVNVKVFIIIAVFFI 247
DB 180 TNFICVAIP-LNFSAILILSNCLVIRQLYRN-----KONENYPNVKKALINLLVTTGII 234
QY 248 CFVPHFARIPTLSQTRDVFDCDAENTLFFVKESTLWLTSLNACLDPFFYFFLKSPFN 307
DB 235 CFVPHVIRIPTLSQTRDVFDCDAENTLFFVKESTLWLTSLNACLDPFFYFFLKSPFN 294
QY 308 SLI-----SMLKCPNSA 319
DB 295 KVTETASPKEKTKAQRKELRCENNA 319

RESULT 9
GP34_MOUSE
ID GP34_MOUSE STANDARD; PRT; 375 AA.
AC Q9RIK6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Probable G protein-coupled receptor GPR34.
GN GPR34.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99326137; PubMed=10395919;
RA Schoneberg T., Schulz A., Grosse R., Schade R., Henklein P.,
RA Schultz G., Gudermann T.;
RT "A novel subgroup of class I G-protein-coupled receptors.";
RL Biochim. Biophys. Acta 1446:57-70(1999).
CC -!- FUNCTION: ORPHAN RECEPTOR.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).
CC -!- TISSUE SPECIFICITY: BROADLY EXPRESSED.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC      EMBL; AF081916; AAD50550.2; -.
CC      MGD; MGI:1346334; Gpr34.
CC      InterPro; IPR000276; GPCR_Rhodpsn.
CC      Pfam; PF00001; 7tm_1; 1.
CC      PRINTS; PR00317; GPCR_Rhodopsin.
CC      PROSITE; PS00237; G-PROTEIN RECEPTOR FL 1; 1.
CC      PROSITE; PS00262; G-PROTEIN RECEPTOR FL 2; 1.
CC      KW      Receptor; G-protein coupled receptor; Transmembrane; Glycoprotein.
CC      FT      DOMAIN 1 54
CC      FT      DOMAIN 55 75
CC      FT      TRANSMEM 76 81
CC      FT      DOMAIN 82 102
CC      FT      TRANSMEM 103 121
CC      FT      DOMAIN 122 142
CC      FT      TRANSMEM 143 164
CC      FT      DOMAIN 165 185
CC      FT      TRANSMEM 186 209
CC      FT      DOMAIN 210 230
CC      FT      TRANSMEM 231 262
CC      FT      DOMAIN 263 283
CC      FT      TRANSMEM 284 303
CC      FT      DOMAIN 304 324
CC      FT      TRANSMEM 325 375
CC      FT      DOMAIN 376 431
CC      FT      TRANSMEM 432 481
CC      FT      DISULFID 120 197
CC      FT      CARBOHYD 21 29
CC      FT      CARBOHYD 29 35
CC      FT      CARBOHYD 35 35
CC      FT      CARBOHYD 193 193
CC      FT      CARBOHYD 288 288
CC      SEQUENCE 375 AA; 43173 MW; C04E1C1A52521045 CRC64;
CC
CC      Query Match      23.1%; Score 411.5; DB 1; Length 375;
CC      Best Local Similarity 32.0%; Pred No. 5.3e-22;
CC      Matches 101; Conservative 52; Mismatches 154; Indels 9; Gaps 7;
CC
CC      QY      2 QAVDNLTSAPGNTSLCTDYKITQVLFLLYTVFFVGLINGLAMRIFQIRKSNFI- 60
CC      Db      25 QASQNFSGVNPVNTS-CPMDEKLLSVLTFTFSVFLVGLVGNITIALYVFLGIHRKRSIQ 83
CC
CC      QY      61 IFLKNTVLSLLMLTFFPKILSDAKLGTGRLTFVCOVTSVIFVFWYISIFLGLITI 120
CC      Db      84 IYLLNVAVADLLIICLFRIMYHINQNKWTGLVILCKVGTFTFMNMYISIIILGLISL 143
CC
CC      QY      121 DRYQKTRTPFTSNPKNLLGAKILSWIAPFMLLSLENMILTRQPRDRKNVKKCSFLKS 180
CC      Db      144 DRYKINRSIQORRAITTKQSIYVCCIVWT-VALAGFLTMIILTKKGHNSTWCFHYRD 202
CC
CC      QY      181 EFLGLVHVEIVNYICOVIFNIFLIVICVYLTITKELYR-SYVTR--GVGKVPKKVNVK 237
CC      Db      203 RINAKGEAIFNVLVVMFWLFLIILSIYKIGKLLRIKRSKFNPSNGKIATARN-- 260
CC
CC      QY      238 VFIIIAVFICFPVPHFARIPYLTISQTRDVEDFTAENTLFVYKKESTLMLTSLNACLDPFI 297
CC      Db      261 SFVILIIICFPVPHFARFVIYSSQL-NVSSCYWKEIHKNTIMLVFSSFNCLDPVM 319
CC
CC      QY      298 YFFLCKSPNLSIML 313
CC      Db      320 YFLMSSNIRKIMCOLL 335

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## RESULT 10

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ID      GP34 HUMAN STANDARD; PRT; 381 AA.
AC      Q95853; O95853;
DT      16-OCT-2001 (Rel. 40, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      15-SEP-2003 (Rel. 42, Last annotation update)
DE      Probable G protein-coupled receptor GPR34.

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GN      GPR34.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Fetal brain;
RX      MEDLINE=99326137; PubMed=10395919;
RA      Schoneberg T., Schulz A., Grosse R., Schade R., Henklein P.,
RA      Schultz G., Gudermann T.;
RT      "A novel subgroup of class I G-protein-coupled receptors.";
RL      Biochim. Biophys. Acta 1446:57-70(1999).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=99156852; PubMed=10036181;
RA      Marchese A., Sawdargo M., Nguyen T., Cheng R., Heng H.H., Nowak T.,
RA      Im D.-S., Lynch K.R., George S.R., O'Dowd B.F.;
RT      "Discovery of three novel orphan G-protein-coupled receptors.";
RL      Genomics 56:12-21(1999).
RN      [3]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=20434921; PubMed=10982042;
RA      Jacobi F.K., Broghammer M., Pesch K., Zrenner E., Berger W.,
RA      Weindl A., Pusch C.M.;
RT      "Physical mapping and exclusion of GPR34 as the causative gene for
RT      congenital stationary night blindness type 1.";
RL      Hum. Genet. 107:89-91(2000).
RN      [4]
RP      SEQUENCE FROM N.A.
RX      TISSUE=Placenta;
RC      Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA      Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,
RA      Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,
RA      Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,
RA      Wakamatsu A., Nakamura Y., Nagahara K., Masuho Y., Oshima A.;
RT      "NEDO human cDNA sequencing project.";
RL      Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN      [5]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Placenta;
RX      MEDLINE=22388257; PubMed=12477932;
RA      Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klautner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA      Altschul S.P., Zeeberg S., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA      Hootkins R.F., Jordan H., Moore T., Max J., Wang J., Hsieh P.,
RA      Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA      Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA      Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA      Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaney S.J.,
RA      Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA      Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA      Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA      Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA      Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA      Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA      Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT      "Generation and initial analysis of more than 15,000 full-length
RT      human and mouse cDNA sequences.";
RL      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC      -!- FUNCTION: ORPHAN RECEPTOR.
CC      -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC      -!- TISSUE SPECIFICITY: BROADLY EXPRESSED.
CC      -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC -----
CC EMBL; AF039686; AAD50531.1; -
DR EMBL; AF118670; AAD17248.1; -
DR EMBL; AK02780; BAB55362.1; -
DR EMBL; BC020678; AAR20678.1; -
DR EMBL; BC020678; AAR20678.1; -
DR MIW; 300241; -
DR GO; GO:0005887; C: integral to plasma membrane; TAS.
DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. .; TAS.
DR InterPro; IPR00276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODOPSIN.
DR PROSITE; PS00237; G PROTEIN RECP F1.1; 1.
DR PROSITE; PS00237; G PROTEIN RECP F1.2; 1.
DR PROSITE; PS00262; G PROTEIN RECP F1.3; 1.
KW Receptor; G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 61
FT TRANSMEM 62 82
FT DOMAIN 83 88
FT TRANSMEM 89 109
FT DOMAIN 110 128
FT TRANSMEM 129 149
FT DOMAIN 150 171
FT TRANSMEM 172 192
FT DOMAIN 193 216
FT TRANSMEM 217 237
FT DOMAIN 238 269
FT TRANSMEM 270 290
FT DOMAIN 291 310
FT TRANSMEM 311 331
FT DOMAIN 332 381
FT TRANSMEM 381 440
FT DISULFID 127 204
FT CARBOHYD 28 28
FT CARBOHYD 36 36
FT CARBOHYD 42 42
FT CARBOHYD 200 200
FT CARBOHYD 295 295
FT CONFLICT 181 181
SQ SEQUENCE 381 AA; 43860 MW; 491FC0165E24379 CRC64;

Query Match      23.0%; Score 409.5; DB 1; Length 381;
Best Local Similarity 32.3%; Pred. No. 7.4e-22;
Matches 102; Conservative 53; Mismatches 152; Indels 9; Gaps 7;

QY 2 QAVNLTSPAGTSLCTRDYKTKITQVLPFLYTVLPVGLITNGLAMRIFQIRSKNFI- 60
DB 32 QPPQNFSGATP-NVTTCPMDEKLLSTVLTTSYSVIFVGLVGNIALYVFLGIRKNSIQ 90
QY 61 IFLKNTVSDLLMTLTPFKILSDAKLGTGRLTFVQVTSVIFFTMYISISFLGLITI 120
DB 91 IYLLNVAIDALLFLCPFLRMVHINQKWLGLVCKVVGTLFYNNMVISIILLGFISL 150
QY 121 DRYQKTRPFTKSNPKNLGAKILSVIVNAPMFLSLPNMILNRPDRQKVKKCSFLKS 180
DB 151 DRYIKINRSIQQRKAITTKOSIYVCCIVW-MLALGGFLTWIILTKKGGHNSWCFHYRD 209
QY 181 EFGVLWHEIVNVIQVTFWFLNFIIVICYTLITKELVR-SVATR--GVCKVPRKKVNVK 237
DB 210 KHNAGKAIFNFIIVWFLNFIILISYIKIGKLLIRISKRKSPNSKYATTARN-- 267
QY 238 VFIIIAVFFICFVPHPARIPYITQSQTRDVFDCPAENTLPYKVESTLWFLSLNACLDPFI 297
DB 268 SFIVLIITFTICFVPHAFRPIYIISQL-NVSSCYWKEIVHKTNEIMVLVSFNSCLDPVM 326
QY 298 YFFLCKSPNSLSMWL 313
DB 327 YFLMSSNIRKIMCQL 342
```

RESULT 11

PAFR\_HUMAN

ID\_PAFR\_HUMAN

AC P25105;

STANDARD;

PRF;

342 AA.

DT 01-MAY-1992 (Rel. 22, Created)

DT 01-MAY-1992 (Rel. 22, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotator update)

DE Platelet activating factor receptor (PAF-R).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=92028922; PubMed=1656963;

RA Ye R.D., Prossnitz E.R., Zou A., Cochran C.G.;

RT "Characterization of a human cDNA that encodes a functional receptor for platelet activating factor.";

RL Biochem. Biophys. Res. Commun. 180:105-111(1991).

RN [2]

RP SEQUENCE FROM N.A.

RX TISSUE=Leukocyte;

RX MEDLINE=92041873; PubMed=1657923;

RA Nakamura M., Honda Z., Izumi T., Sakanaka C., Mutoh H., Minami M., Bito H., Seyama Y., Matsumoto T., Noma M., Shimizu T.;

RT "Molecular cloning and expression of platelet-activating factor receptor from human leukocytes.";

RL J. Biol. Chem. 266:20400-20405(1991).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=92250505; PubMed=1374385;

RA Kunz D., Gerard N.P., Gerard C.;

RT "The human leukocyte platelet-activating factor receptor. cDNA cloning, cell surface expression, and construction of a novel epitope-bearing analog.";

RL J. Biol. Chem. 267:9101-9106(1992).

RN [4]

RP SEQUENCE FROM N.A.

RX MEDLINE=92347886; PubMed=1322356;

RA Seyfried C.E., Schweickart V.L., Godiska R., Gray P.W.;

RT "The human platelet-activating factor receptor gene (PTAFR) contains no introns and maps to chromosome 1.";

RL Genomics 13:832-834(1992).

RN [5]

RP SEQUENCE FROM N.A.

RX TISSUE=Heart;

RX MEDLINE=93112021; PubMed=1281995;

RA Sugimoto T., Tsuchinouchi H., McGregor C.G., Mutoh H., Shimizu T., Kurachi Y.;

RT "Molecular cloning and characterization of the platelet-activating factor receptor gene expressed in the human heart.";

RL Biochem. Biophys. Res. Commun. 189:617-624(1992).

RN [6]

RP SEQUENCE FROM N.A.

RX Behal R.H., Debussche M.S., Olson M.S.;

RL Submitted (XX-1992) to the EMBL/GenBank/DBJ databases.

RN [7]

RP SEQUENCE FROM N.A.

RX MEDLINE=93192035; PubMed=838507;

RA Chase P.B., Halonen M., Regan J.W.;

RT "Cloning of a human platelet-activating factor receptor gene: evidence for an intron in the 5'-untranslated region.";

RL Am. J. Respir. Cell Mol. Biol. 8:240-244(1993).

RN [8]

RP VARIANTS ASP-224 AND SER-338.

RX MEDLINE=9318093; PubMed=10391209;

RA Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N., Shaw N., Lane C.R., Lim E.P., Kalyanaram N., Nemes J., Ziaugra L., Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q., Lander E.S.;

RT "Characterization of single-nucleotide polymorphisms in coding regions of human genes.";

RL Nat. Genet. 22:231-238(1999).

RN [9]

RP ERRATUM.

RA Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N.,



Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L.,  
 Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,  
 Lander E.S.,  
 Nat. Genet. 23:373-373 (1999).  
 CC -!- FUNCTION: RECEPTOR FOR PLATELET ACTIVATING FACTOR, A CHEMOTACTIC  
 CC PHOSPHOLIPID MEDIATOR THAT POSSESSES POTENT INFLAMMATORY, SMOOTH-  
 CC MUSCLE CONTRACTILE AND HYPOTENSIVE ACTIVITY. SEEM TO MEDIATE ITS  
 CC ACTION VIA A G PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-  
 CC CALCIUM SECOND MESSENGER SYSTEM.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC  
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 CC  
 CC EMBL; M80436; AAA60001.1; -  
 CC EMBL; M76674; AAA60002.1; -  
 CC EMBL; D10202; BAA01050.1; -  
 CC EMBL; M88177; AAA60214.1; -  
 CC EMBL; S52624; AAB24695.2; -  
 CC EMBL; L07334; AAA60108.1; -  
 CC EMBL; S56396; AAB25755.1; -  
 CC PIR; A40191; A40191  
 CC Genew; HGNC:9582; PAFR.  
 CC  
 CC MIM; 173393; -  
 CC GO; GO:0005887; C:integral to plasma membrane; TAS.  
 CC GO; GO:0004992; P:platelet activating factor receptor activity; TAS.  
 CC GO; GO:0006960; P:antimicrobial humoral response (sensu Inver. . . ; TAS.  
 CC GO; GO:0006935; P:chemotaxis; TAS.  
 CC GO; GO:0007186; P:G-protein coupled receptor protein signalin. . . ; TAS.  
 CC GO; GO:0006955; P:immune response; TAS.  
 CC GO; GO:0006954; P:inflammatory response; TAS.  
 CC GO; GO:0009405; P:phagocytosis; TAS.  
 CC InterPro; IPR000276; GPCR\_Rhodopsn.  
 CC Pfam; PF00001; 7tm1.1.  
 CC PRINTS; PR00237; GPCRHOPOPSN.  
 CC PROSITE; PS00237; G-PROTEIN RECP\_F1\_1; 1.  
 CC PROSITE; PS00262; G-PROTEIN RECP\_F1\_2; 1.  
 CC G-protein coupled receptor; Transmembrane; Glycoprotein; Chemotaxis;  
 CC Polymorphism.  
 KW Polymorphism.  
 FT DOMAIN 1 16 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 17 38 1 (POTENTIAL).  
 FT DOMAIN 39 54 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 55 74 2 (POTENTIAL).  
 FT DOMAIN 75 91 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 92 113 3 (POTENTIAL).  
 FT DOMAIN 114 133 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 134 155 4 (POTENTIAL).  
 FT DOMAIN 156 184 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 185 205 5 (POTENTIAL).  
 FT DOMAIN 206 233 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 234 254 6 (POTENTIAL).  
 FT DOMAIN 255 276 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 277 296 7 (POTENTIAL).  
 FT DOMAIN 297 342 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 90 173 BY SIMILARITY.  
 FT CARBOHYD 169 169 A -> D (IN dBSNP:5938).  
 FT VARIANT 224 224 /FTIDVAR\_011851.  
 FT VARIANT 338 338 N -> S (IN dBSNP:5939).  
 FT VARIANT 338 338 /FTIDVAR\_011852.  
 FT CONFLICT 38 38 L -> P (IN REF. 6).  
 FT CONFLICT 66 66 F -> L (IN REF. 6).  
 FT CONFLICT 95 95 C -> R (IN REF. 6).  
 FT CONFLICT 227 228 KR -> TG (IN REF. 4).  
 FT CONFLICT 227 228 KR -> TT (IN REF. 6).  
 FT CONFLICT 247 247 P -> A (IN REF. 6).  
 FT CONFLICT 316 316 K -> N (IN REF. 5).

SQ SEQUENCE 342 AA; 39203 MW; 890073C9EBA79228 CRC64;  
 Query Match 22.2%; Score 394; DB 1; Length 342;  
 Best Local Similarity 32.6%; Pred. No. 8e-21;  
 Matches 107; Conservative 61; Mismatches 134; Indels 26; Gaps 10;  
 QY 11 PONTSLCTRDYKIVTQVLPPLLYTVLFFVGLTNGLAMRIPQIR--SKSNFI--IFLKNTV 67  
 DB 3 PHDSHMDSEPRYT--LPIIVYSIIFVLGVANGVLMVFARLYPCKKFKIKFMVNL 60  
 QY 68 ISDLMLITFPFKILSDAKLGTPLRTFVCOVTSVIFYFTWVISIFLGLITIDRYQKTT 127  
 DB 61 MADMLFLTLPLWIVYQNGNWILPKELCNVAGCLFINTYCSVAFGLVITYNRFQAVT 120  
 QY 128 RPKTSNPKNLGAKILSVIIVW----AFMFLSLPMLNTRQPRDK---NVKCCFLK 179  
 DB 121 REIKTAQANTRKRGISLSLVIWVAIVGAASYFLIDS---TNTVPDSAGSNVTRC-FEH 176  
 QY 180 SEFGLVWHEIVNYICQVFWINFLIVICVTLITKELYRSVVRTRGVGKVRKKNVXVF 239  
 DB 177 YEKGSVPVLIHIFIVFSFVFLVLLFCNLVIRTLMLQPVQQRNAEVRRLMW-VC 235  
 QY 240 IIAVFFICFVFFHFAPIYTLSTQTRVDFCTAENTLKYKSTLWLSNACLDPIFYF 299  
 DB 236 TVLAVFIIICFVPHVHVQLPWLAEI-GPQDSKFKHQAINDAHQVTLICLLSTNCVLDPIVC 294  
 QY 300 FLCKSFEN-----SLISMLKCPNSAT 320  
 DB 295 FLTKFKRHLEKFKYSMRSSKCSRAIT 322  
 RESULT 12  
 PAFR CAVPO  
 ID PAFR CAVPO STANDARD; PRT; 342 AA.  
 AC P21556;  
 DT 01-MAY-1991 (Rel. 18, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE Platelet activating factor receptor (PAF-R).  
 GN PAFR.  
 OS Cavia porcellus (Guinea pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Caviidae; Cavia.  
 OX NCBI\_TaxID=10141;  
 RN [1]  
 SEQUENCE FROM N.A.  
 RP TISSUE=Lung;  
 RX MEDLINE=91101726; PubMed=1846231;  
 RA Honda Z.-I., Nakamura M., Miki I., Minami M., Watanabe T., Seyama Y.,  
 RA Okado H., Toh H., Ito K., Miyamoto T., Shimizu T.  
 RT "Cloning by functional expression of platelet-activating factor  
 RL receptor from guinea-pig lung."  
 RL Nature 349:342-346 (1991).  
 CC -!- FUNCTION: RECEPTOR FOR PLATELET ACTIVATING FACTOR, A CHEMOTACTIC  
 CC PHOSPHOLIPID MEDIATOR THAT POSSESSES POTENT INFLAMMATORY, SMOOTH-  
 CC MUSCLE CONTRACTILE AND HYPOTENSIVE ACTIVITY. SEEM TO MEDIATE ITS  
 CC ACTION VIA A G PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-  
 CC CALCIUM SECOND MESSENGER SYSTEM.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC  
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 CC  
 CC EMBL; X56736; CAA40060.1; -  
 CC PIR; S13638; S13638.  
 CC InterPro; IPR000276; GPCR\_Rhodopsn.  
 CC Pfam; PF00001; 7tm1.1.



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QY 282 STLWLTSLNACLDPTLYFFLCKSFNSLSMLKCPNSATSLSDNRKKEQDGPNEPTP 341
Db 282 FTVCLMNFCCMDPTLYFFLCKSFNSLSMLKCPNSATSLSDNRKKEQDGPNEPTQ 350
QY 342 M 342
Db 351 M 351

RESULT 14
ID CLT2_PIG STANDARD; PRT; 345 AA.
AC Q95N03;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cysteinyln leukotriene receptor 2 (CysLTR2).
GN CYSLTR2 OR CYSLTR2.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Kamohara M., Takasaki J., Matsumoto M., Matsumoto S., Saito T.,
RA Chishi T., Soga T., Matsushime H., Furuichi K.;
RT "Characterization of the cloned rat and porcine cysteinyl leukotriene
RL Submitter (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC mediated via a G-protein that activates a phosphatidylinositol-
CC calcium second messenger system (by similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC
CC EMBL; AB052662; BAB60817.1;
DR InterPro; IPR004071; Cysleuk receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1_1;
DR PRINTS; PR01533; CYSLTR2RCPT.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; FALSE_NEG.
DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 43 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 44 64 1 (POTENTIAL).
FT DOMAIN 65 73 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 74 94 2 (POTENTIAL).
FT DOMAIN 95 124 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 125 145 3 (POTENTIAL).
FT DOMAIN 146 154 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 155 175 4 (POTENTIAL).
FT DOMAIN 176 205 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 206 226 5 (POTENTIAL).
FT DOMAIN 227 246 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 247 267 6 (POTENTIAL).
FT DOMAIN 268 287 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 288 308 7 (POTENTIAL).
FT DOMAIN 309 345 CYTOPLASMIC (POTENTIAL).
FT DISULFID 112 188 BY SIMILARITY.
FT CARBOHYD 20 20 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 29 29 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 184 184 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 345 AA; 39410 MW; 5D1B1FB98BB95905 CRC64;
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Query Match 20.6%; Score 367; DB 1; Length 345;
Best Local Similarity 29.0%; Pred. No. 6.le-19;
Matches 93; Conservative 72; Mismatches 134; Indels 22; Gaps 9;

QY 1 MQAVDNLTSAPGNLSLCTRDYKITQVLFPLLYTLVFFVGLITNGLAMRIFFOIRSKSNFI 60
Db 17 MEFNSTLGNHNSRSCCTTENPK--REFYPIVLYVIFINGALNGFSIVVPLKPYKSTSV 74

QY 61 -PLKNTVISDLMLITFPFKI-----LSDAKLGTGRLPTFCQVTSVIFVTMTWISIF 114
Db 75 NVFEMNLAIISDLLFTITLFRVYVYLRGNSXIFGDT-----CRMSYSMYNMYSSYIF 129

QY 115 LGLITIDRYQKTRPPKTSNPKNLGAKILSVVIAFWAFLLSPNMLITNRPDRKNVKK 174
Db 130 LTVLVVVRFLATVHPRLHTTSIKNANLLCGVIN--IFIMASSTVLLKNGSEQKDNVTL 187

QY 175 CSFLKSEFGLVWHEIVNYICQVI-FWINEFLIVVYTLITKELYRSYVTRGVKVPKPK 233
Db 188 CLELNSN-KVTKLTNNYVALVGVFLPFGTSLICYLLIIRALLKVEVPESGL-RLSHRK 245

QY 234 VNVKVFIIIAVFICFPFHPIPVYTLISQTRDVEDCTAENTLFVVKESSTLWLTSLNACL 293
Db 246 ALITVIALIIIFLLCLPFPYHVTHTLLEWKAD----KCKORLHKAVAVTLALAANSCF 301

QY 294 DPFYFFLCKSFNSLSMLK 314
Db 302 NPFLYFAGENFKDLKSLR 322
```

## RESULT 15

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PAFR_MOUSE STANDARD; PRT; 341 AA.
ID PAFR_MOUSE Q62035;
AC DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Platelet activating factor receptor (PAF-R).
GN PAFR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/Sv;
RX MEDLINE=96239129; PubMed=8670084;
RA Ishii S., Matsuda Y., Nakamura M., Waga I., Kume K., Izumi T.,
RA Noma M., Shimizu T.;
RT "A murine platelet-activating factor receptor gene: cloning,
RT chromosomal localization and up-regulation of expression by
RT lipopolysaccharide in peritoneal resident macrophages.";
RL Biochem J 314:671-678(1996)
CC -!- FUNCTION: RECEPTOR FOR PLATELET ACTIVATING FACTOR, A CHEMOTACTIC
CC PHOSPHOLIPID MEDIATOR THAT POSSESSES POTENT INFLAMMATORY, SMOOTH-
CC MUSCLE CONTRACTIONS AND HYPOTENSIVE ACTIVITY. SEEM TO MEDIATE ITS
CC ACTION VIA A G PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-
CC CALCIUM SECOND MESSENGER SYSTEM.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC
CC EMBL; D50872; BAA09468.1;
DR PIR; S63666; S63666.
DR MGD; MGI:106066; Ptafr.
DR InterPro; IPR000276; GPCR_Rhodpsn.
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